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April 28, 1999

Box Patent Application

Assistant Commissioner for Patents
Washington, D.C. 20231

Re: U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed: Herewith
For: Nucleic Acid Molecules and Other Molecules Associated with the Phosphogluconate Pathway
Inventors: Nordine CHEIKH *et al.*
Atty. Docket: 04983.0031.US01/38-21(15365)B

Sir:

The following documents are forwarded herewith for appropriate action by the U.S. Patent and Trademark Office:

1. Utility Patent Application Transmittal (PTO/SB/05);

2. U.S. Utility Patent Application entitled:

Nucleic Acid Molecules and Other Molecules Associated with the Phosphogluconate Pathway

and naming as inventors:

Nordine Cheikh, Jingdong Liu, and Virginia M. Peschke

the application consisting of:

a. A specification containing:

(i) 242 pages of a description prior to the claims;

(ii) 5 pages of claims (9 claims);

(iii) a one (1) page abstract; and

(iv) 237 pages of a sequence listing;

3. A computer readable disk copy of the sequence listing;

4. Statement Regarding Sequence Submission; and

5. Two (2) return postcards.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

This application claims priority under 35 U.S.C §119(e) and/or 35 U.S.C §120 of applications No. 60/083,390, filed April 29, 1998, which is herein incorporated by reference in its entirety.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the sequence listing and the computer readable copy of the sequence listing submitted herewith in the above application are the same.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)

Enclosures

PTO/SB/05 (2/98)
Approved for use through 09/30/00. OMB 0651-0032
Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE

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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	04983.0031.US01/38-21(15365)B
First Named Inventor or Application Identifier	CHEIKH
Title	Nucleic Acid Molecules And Other Molecules Associated With the Phosphogluconate Pathway
Express Mail Label No.	

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

1. ☐ *Fee Transmittal Form (Form PTO-1082)
(Submit an original and a duplicate for fee processing)
2. ☒ Specification [*Total Pages* 248]
(preferred arrangement set forth below)
- Descriptive title of the Invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R&D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claims
- Abstract of the Disclosure
3. ☐ Drawing(s) *(35 USC 113)* [*Total Sheets*]
4. Oath or Declaration [*Total Pages*]
a. ☐ Newly executed (original or copy)
b. ☐ Copy from a prior application (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)
[Note Box 5 below]
i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).
5. ☐ Incorporation By Reference *(useable if Box 4b is checked)*
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
6. ☐ Microfiche Computer Program *(Appendix)*
7. Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)
a. ☒ Computer Readable Copy
b. ☒ Paper Copy (identical to computer copy)
c. ☒ Statement verifying identity of above copies

jc625 U.S. PTO
09/300482
04/28/99

ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & document(s))
9. ☐ 37 CFR 3.73(b) Statement *(when there is an assignee)* ☐ Power of Attorney
10. ☐ English Translation Document *(if applicable)*
11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
12. ☐ Preliminary Amendment
13. ☒ Return Receipt Postcard (MPEP 503) (Two)
(should be specifically itemized)
14. ☐ *Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired
15. ☐ Certified Copy of Priority Document(s)
(if foreign priority is claimed)
16. ☐ Other:

*NOTE FOR ITEMS 1 & 14: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

17. **If a CONTINUING APPLICATION,** *check appropriate box and supply the requisite information:*
☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No: /
Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS

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Signature		*Date*	*April 28, 1999*

Burden Hour Statement: This form is estimated to take 0.2 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231.

NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH THE PHOSPHOGLUCONATE PATHWAY

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. § 119(e) to application serial no. 60/083,390, filed April 29, 1998, which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention is in the field of plant biochemistry. More specifically the invention relates to nucleic acid sequences from plant cells, in particular, nucleic acid sequences from maize and soybean plants associated with the phosphogluconate pathway in plants. The invention encompasses nucleic acid molecules that encode proteins and fragments of proteins. In addition, the invention also encompasses proteins and fragments of proteins so encoded and antibodies capable of binding these proteins or fragments. The invention also relates to methods of using the nucleic acid molecules, proteins and fragments of proteins and antibodies, for example for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants.

BACKGROUND OF THE INVENTION

I. PHOSPHOGLUCONATE PATHWAY

The phosphogluconate pathway (OPPP) (also known as the oxidative pentose phosphate pathway, pentose phosphate shunt, or Warburg-Dickens pathway) is one of the two major pathways in plants by which carbohydrates may be ultimately degraded into CO_2, the other being glycolysis followed by the TCA cycle (Brownleader *et al.*, In: *Plant Biochemistry* Academic Press, New York, pp. 111-141, (1997), the entirety of which is herein incorporated by reference). It has been reported that the OPPP generally accounts for 10-15% of the carbohydrate oxidation

in cells (apRees In: *The Biochemistry of Plants Vol 3*:1-42, (1980), the entirety of which is herein incorporated by reference). It has been reported that the primary purposes of the OPPP is production of NADPH for use in biosynthetic reactions and the production of a ribose-5-phosphate for use in nucleic acid biosynthesis (Turner and Turner, In: *Biochemistry of Plants - A Comprehensive Treatise Vol 2*:279-316, (1980), the entirety of which is herein incorporated by reference). The subcellular localization of this pathway has been reported to differ between species, cell type, and plastid type being investigated. For example, reported cellular fractionation experiments in spinach leaf cells showed all enzymes of the phosphogluconate pathway were found in chloroplasts, but that only the first two enzymes of that pathway are present in the cytosol (Schnarrenberger *et al.*, *Plant Physiol. 108*:609-614, (1995), the entirety of which is herein incorporated by reference).

In general, OPPP can be divided into two parts, oxidative (the reactions leading up to ribulose-5-phosphate), and non-oxidative (*e.g.* Williams, *Trends Biochem. Sci. 5*:315-320, (1980); apRees, In: *Encyclopedia of Plant Physiology Vol 18* pp.391-417, (1985), all of which references are incorporated herein in their entirety).

The first reported reaction of OPPP is the conversion of glucose-6-phosphate by glucose-6-phosphate dehydrogenase (G6PDH; EC 1.1.1.49) to 6-phosphogluconolactone. The hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate can occur in a nonenzymatically manner or be catalyzed by a lactonase. This reaction is not at equilibrium and is irreversible (Ashihara and Komamine, *Plant Sci. Lett. 2*:331-337 (1974), the entirety of which is herein incorporated by reference; Turner and Turner, In: *Biochemistry of Plants - A Comprehensive Treatise Vol 2*:279-316, (1980)). The hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate is reported to be a critical regulatory step in the phosphogluconate pathway. The hydrolysis of 6-

phosphogluconolactone to 6-phosphogluconate has been reported to respond to the concentration of glucose-6-phosphate as well as the NADPH/NADP+ ratio. Inhibition of the hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate by NADPH is consistent with the function of OPPP to provide NADPH (apRees, In: *The Biochemistry of Plants Vol 3*:1-42, (1980)). cDNA clones for G6PDH have been isolated from several plants including alfalfa (Fahrendorf *et al.*, *Plant Mol. Biol. 28*: 885-900, (1995), the entirety of which is herein incorporated by reference) and potato (Graeve *et al.*, *Plant J. 5*:353-361, (1994), the entirety of which is herein incorporated by reference).

6-phosphogluconate is dehydrogenated to ribulose-5-phosphate, NADPH, and CO_2 in an irreversible reaction catalyzed by 6-phosphogluconate dehydrogenase (6PGDH; EC1.1.1.44). A cDNA clone for 6PGDH has been isolated from alfalfa (Fahrendorf *et al.*, *Plant Mol Biol 28*: 885-900, (1995)). The first two steps of the OPPP are the only reported oxidation reactions in that pathway. Other reactions within OPPP serve to regenerate glucose-6-phosphate, as well as producing intermediates such as ribose-5-phosphate that are ultilized in nucleic acid biosynthesis.

Ribulose-5-phosphate may be metabolized in one of two pathways. Ribose-5-phosphate isomerase (EC 5.3.1.6) catalyzes the conversion of ribulose-5-phosphate to ribose-5-phosphate, while ribulose-5-phosphate-3-epimerase (also known as pentose-5-phosphate-3-epimerase; EC 5.1.3.1) catalyzes the conversion of ribulose-5-phosphate to xylulose-5-phosphate. Transketolase (EC 2.2.1.1) catalyzes the conversion of ribulose-5-phosphate and xylulose-5-phosphate into sedheptulose-7-phosphate and 3-phosphoglyceraldehyde. Transaldolase (EC 2.2.1.2) catalyzes the conversion of sedheptulose-7-phosphate and 3-phosphoglyceraldehyde into erythrose-4-phosphate and fructose-6-phosphate.

Erythrose-4-phosphate is a substrate associated with the biosynthesis of lignin (Salisbury and Ross, *Plant Physiology,* Wadsworth Publishing Company, Belmont CA, (1978), the entirety of which is herein incorporated by reference), or the production of aromatic amino acids via the shikimate pathway (Schnarrenberger *et al., Plant Physiol. 108*:609-614, (1995), the entirety of which is herein incorporated by reference). Clones for potato transaldolase (Moehs *et al., Plant Mol. Biol. 32*:447-452, (1996), the entirety of which is herein incorporated by reference); spinach transketolase (Flechner *et al., Plant Mol. Biol. 32*:475-484, (1996), the entirety of which is herein incorporated by reference); potato ribulose-5-phosphate-3-epimerase (Teige *et al., FEBS Lett.* 377:349-352, (1995), the entirety of which is herein incorporated by reference); and spinach ribulose-5-phosphate-3-epimerase (Nowitzki *et al., Plant Mol. Biol. 29*:1279-1291, (1995), the entirety of which is herein incorporated by reference) have been reported.

Fructose-6-phosphate may enter glycolysis (apRees, In: *The Biochemistry of Plants Vol 3*:1-42, (1980)). Fructose-6-phosphate can also be converted to glucose-6-phosphate via phosphohexose isomerase (also known as phosphoglucoisomerase)(EC5.3.1.9). Glucose-6-phosphate can be recycled in the OPPP pathway or be utilized during the synthesis of polysaccharides.

Transketolase (EC2.2.1.1) can catalyze the conversion of erythrose-4-phosphate and xylulose-5-phosphate to fructose 6-phosphate and 3-phosphoglyceraledehyde. Likewise, fructose 6-phosphate and 3-phosphoglyceraledehyde may be used in reactions as described above.

II. EXPRESSED SEQUENCE TAG NUCLEIC ACID MOLECULES

Expressed sequence tags, or ESTs are randomly sequenced members of a cDNA library (or complementary DNA)(McCombie *et al., Nature Genetics 1:*124-130 (1992); Kurata *et al.,*

Nature Genetics 8: 365-372 (1994); Okubo, *et al. Nature Genetics 2:* 173-179 (1992), all of which references are incorporated herein in their entirety). The randomly selected clones comprise insets that can represent a copy of up to the full length of a mRNA transcript.

Using conventional methodologies, cDNA libraries can be constructed from the mRNA (messenger RNA) of a given tissue or organism using poly dT primers and reverse transcriptase (Efstratiadis *et al., Cell 7*:279-288 (1976), the entirety of which is herein incorporated by reference; Higuchi *et al., Proc. Natl. Acad. Sci. (U.S.A.) 73*:3146-3150 (1976), the entirety of which is herein incorporated by reference; Maniatis *et al., Cell 8*:163-182 (1976) the entirety of which is herein incorporated by reference; Land *et al., Nucleic Acids Res. 9*:2251-2266 (1981), the entirety of which is herein incorporated by reference; Okayama *et al., Mol. Cell. Biol. 2*:161-170 (1982), the entirety of which is herein incorporated by reference; Gubler *et al., Gene 25*:263-269 (1983), the entirety of which is herein incorporated by reference).

Several methods may be employed to obtain full-length cDNA constructs. For example, terminal transferase can be used to add homopolymeric tails of dC residues to the free 3' hydroxyl groups (Land *et al., Nucleic Acids Res. 9*:2251-2266 (1981), the entirety of which is herein incorporated by reference). This tail can then be hybridized by a poly dG oligo which can act as a primer for the synthesis of full length second strand cDNA. Okayama and Berg, *Mol. Cell. Biol. 2:* 161-170 (1982), the entirety of which is herein incorporated by reference, report a method for obtaining full length cDNA constructs. This method has been simplified by using synthetic primer-adapters that have both homopolymeric tails for priming the synthesis of the first and second strands and restriction sites for cloning into plasmids (Coleclough *et al., Gene 34*:305-314 (1985), the entirety of which is herein incorporated by reference) and bacteriophage vectors (Krawinkel *et al., Nucleic Acids Res. 14*:1913 (1986), the entirety of which is herein

incorporated by reference; Han *et al.*, *Nucleic Acids Res. 15*:6304 (1987), the entirety of which is herein incorporated by reference).

These strategies have been coupled with additional strategies for isolating rare mRNA populations. For example, a typical mammalian cell contains between 10,000 and 30,000 different mRNA sequences (Davidson, *Gene Activity in Early Development*, 2nd ed., Academic Press, New York (1976). The number of clones required to achieve a given probability that a low-abundance mRNA will be present in a cDNA library is $N = (\ln(1-P))/(\ln(1-1/n))$ where N is the number of clones required, P is the probability desired, and 1/n is the fractional proportion of the total mRNA that is represented by a single rare mRNA (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press (1989), the entirety of which is herein incorporated by reference).

A method to enrich preparations of mRNA for sequences of interest is to fractionate by size. One such method is to fractionate by electrophoresis through an agarose gel (Pennica *et al.*, *Nature 301*:214-221 (1983), the entirety of which is herein incorporated by reference). Another such method employs sucrose gradient centrifugation in the presence of an agent, such as methylmercuric hydroxide, that denatures secondary structure in RNA (Schweinfest *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 79*:4997-5000 (1982), the entirety of which is herein incorporated by reference).

A frequently adopted method is to construct equalized or normalized cDNA libraries (Ko, *Nucleic Acids Res. 18*:5705-5711 (1990), the entirety of which is herein incorporated by reference; Patanjali, S. R. *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:1943-1947 (1991), the entirety of which is herein incorporated by reference). Typically, the cDNA population is normalized by subtractive hybridization (Schmid *et al.*, *J. Neurochem. 48*:307-312 (1987) the entirety of which

is herein incorporated by reference; Fargnoli *et al.*, *Anal. Biochem. 187*:364-373 (1990) the entirety of which is herein incorporated by reference; Travis *et al.*, *Proc. Natl. Acad. Sci (U.S.A.) 85*:1696-1700 (1988) the entirety of which is herein incorporated by reference; Kato, *Eur. J. Neurosci. 2*:704-711 (1990); and Schweinfest *et al.*, *Genet. Anal. Tech. Appl. 7*:64-70 (1990), the entirety of which is herein incorporated by reference). Subtraction represents another method for reducing the population of certain sequences in the cDNA library (Swaroop *et al.*, *Nucleic Acids Res. 19*:1954 (1991), the entirety of which is herein incorporated by reference).

ESTs can be sequenced by a number of methods. Two basic methods may be used for DNA sequencing, the chain termination method of Sanger *et al., Proc. Natl. Acad. Sci. (U.S.A.) 74:* 5463-5467 (1977), the entirety of which is herein incorporated by reference, and the chemical degradation method of Maxam and Gilbert, *Proc. Nat. Acad. Sci. (U.S.A.) 74:* 560-564 (1977), the entirety of which is herein incorporated by reference. Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods 2:* 20-26 (1991), the entirety of which is herein incorporated by reference; Ju *et al., Proc. Natl. Acad. Sci. (U.S.A.) 92:* 4347-4351 (1995), the entirety of which is herein incorporated by reference; Tabor and Richardson, *Proc. Natl. Acad. Sci. (U.S.A.) 92:* 6339-6343 (1995), the entirety of which is herein incorporated by reference). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res. 18*:1415-1419 (1990); Smith,

Nature 349:812-813 (1991); Luckey *et al.*, *Methods Enzymol. 218*:154-172 (1993); Lu *et al.*, *J. Chromatog. A. 680*:497-501 (1994); Carson *et al.*, *Anal. Chem. 65*:3219-3226 (1993); Huang *et al.*, *Anal. Chem 64*:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis 17*:1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17*:1841-1851 (1996); Baba, *Yakugaku Zasshi 117*:265-281 (1997), all of which are herein incorporated by reference in their entirety).

ESTs longer than 150 nucleotides have been found to be useful for similarity searches and mapping (Adams *et al.*, *Science 252*:1651-1656 (1991), herein incorporated by reference). ESTs, which can represent copies of up to the full length transcript, may be partially or completely sequenced. Between 150-450 nucleotides of sequence information is usually generated as this is length of sequence information that is routinely and reliably produced using single run sequence data. Typically, only single run sequence data is obtained from the cDNA library (Adams *et al.*, *Science 252*:1651-1656 (1991). Automated single run sequencing typically results in an approximately 2-3% error or base ambiguity rate (Boguski *et al.*, *Nature Genetics 4*:332-333 (1993), the entirety of which is herein incorporated by reference).

EST databases have been constructed or partially constructed from, for example, *C. elegans* (McCombrie *et al.*, *Nature Genetics 1*:124-131 (1992)), human liver cell line HepG2 (Okubo *et al.*, *Nature Genetics 2*:173-179 (1992)), human brain RNA (Adams *et al.*, *Science 252*:1651-1656 (1991)); Adams *et al.*, *Nature 355*:632-635 (1992)), *Arabidopsis,* (Newman *et al.*, *Plant Physiol.* 106:1241-1255 (1994)); and rice (Kurata *et al.*, *Nature Genetics 8*:365-372 (1994)).

III. SEQUENCE COMPARISONS

A characteristic feature of a protein or DNA sequence is that it can be compared with other known protein or DNA sequences. Sequence comparisons can be undertaken by

determining the similarity of the test or query sequence with sequences in publicly available or proprietary databases ("similarity analysis") or by searching for certain motifs ("intrinsic sequence analysis")(e.g. *cis* elements)(Coulson, *Trends in Biotechnology 12:* 76-80 (1994), the entirety of which is herein incorporated by reference); Birren *et al., Genome Analysis 1*: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York 543-559 (1997), the entirety of which is herein incorporated by reference).

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(http://www.ddbj.nig.ac.jp/); Genebank (http://www.ncbi.nlm.nih.gov/Web/Search/Index.htlm); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (http://www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology 12:* 76-80 (1994); Birren *et al., Genome Analysis 1:* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York 543-559 (1997)).

BLASTN takes a nucleotide sequence (the query sequence) and its reverse complement and searches them against a nucleotide sequence database. BLASTN was designed for speed, not maximum sensitivity, and may not find distantly related coding sequences. BLASTX takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database. BLASTX is useful for sensitive analysis of preliminary (single-pass) sequence data and is

tolerant of sequencing errors (Gish and States, *Nature Genetics 3:* 266-272 (1993), the entirety of which is herein incorporated by reference). BLASTN and BLASTX may be used in concert for analyzing EST data (Coulson, *Trends in Biotechnology 12:* 76-80 (1994); Birren *et al., Genome Analysis 1:* 543-559 (1997)).

Given a coding nucleotide sequence and the protein it encodes, it is often preferable to use the protein as the query sequence to search a database because of the greatly increased sensitivity to detect more subtle relationships. This is due to the larger alphabet of proteins (20 amino acids) compared with the alphabet of nucleic acid sequences (4 bases), where it is far easier to obtain a match by chance. In addition, with nucleotide alignments, only a match (positive score) or a mismatch (negative score) is obtained, but with proteins, the presence of conservative amino acid substitutions can be taken into account. Here, a mismatch may yield a positive score if the non-identical residue has physical/chemical properties similar to the one it replaced. Various scoring matrices are used to supply the substitution scores of all possible amino acid pairs. A general purpose scoring system is the BLOSUM62 matrix (Henikoff and Henikoff, *Proteins 17:* 49-61 (1993), the entirety of which is herein incorporated by reference), which is currently the default choice for BLAST programs. BLOSUM62 is tailored for alignments of moderately diverged sequences and thus may not yield the best results under all conditions. Altschul, *J. Mol. Biol. 36:* 290-300 (1993), the entirety of which is herein incorporated by reference, describes a combination of three matrices to cover all contingencies. This may improve sensitivity, but at the expense of slower searches. In practice, a single BLOSUM62 matrix is often used but others (PAM40 and PAM250) may be attempted when additional analysis is necessary. Low PAM matrices are directed at detecting very strong but

localized sequence similarities, whereas high PAM matrices are directed at detecting long but weak alignments between very distantly related sequences.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25: 351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: ftp.ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet. 9:*180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: ncbi.nlm.nih.gov (directory/pub/macaw).

Sequence motifs are derived from multiple alignments and can be used to examine individual sequences or an entire database for subtle patterns. With motifs, it is sometimes possible to detect distant relationships that may not be demonstrable based on comparisons of primary sequences alone. Currently, the largest collection of sequence motifs in the world is

PROSITE (Bairoch and Bucher, *Nucleic Acid Research 22:* 3583-3589 (1994), the entirety of which is herein incorporated by reference). PROSITE may be accessed via either the ExPASy server on the World Wide Web or anonymous ftp site. Many commercial sequence analysis packages also provide search programs that use PROSITE data.

A resource for searching protein motifs is the BLOCKS E-mail server developed by S. Henikoff, *Trends Biochem Sci. 18:*267-268 (1993), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Nucleic Acid Research 19:*6565-6572 (1991), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Proteins, 17:* 49-61 (1993). BLOCKS searches a protein or nucleotide sequence against a database of protein motifs or "blocks." Blocks are defined as short, ungapped multiple alignments that represent highly conserved protein patterns. The blocks themselves are derived from entries in PROSITE as well as other sources. Either a protein query or a nucleotide query can be submitted to the BLOCKS server; if a nucleotide sequence is submitted, the sequence is translated in all six reading frames and motifs are sought for these conceptual translations. Once the search is completed, the server will return a ranked list of significant matches, along with an alignment of the query sequence to the matched BLOCKS entries.

Conserved protein domains can be represented by two-dimensional matrices, which measure either the frequency or probability of the occurrences of each amino acid residue and deletions or insertions in each position of the domain. This type of model, when used to search against protein databases, is sensitive and usually yields more accurate results than simple motif searches. Two popular implementations of this approach are profile searches (such as GCG program ProfileSearch) and Hidden Markov Models (HMMs)(Krough. *et al., J. Mol. Biol. 235*:1501-1531, (1994); Eddy, *Current Opinion in Structural Biology, 6:*361-365, (1996), both of

which are herein incorporated by reference in their entirety). In both cases, a large number of common protein domains have been converted into profiles, as present in the PROSITE library, or HHM models, as in the Pfam protein domain library (Sonnhammer *et al., Proteins 28*:405-420 (1997), the entirety of which is herein incorporated by reference). Pfam contains more than 500 HMM models for enzymes, transcription factors, signal transduction molecules, and structural proteins. Protein databases can be queried with these profiles or HMM models, which will identify proteins containing the domain of interest. For example, HMMSW or HMMFS, two programs in a public domain package called HMMER (Sonnhammer *et al., Proteins 28*:405-420, (1997)) can be used.

PROSITE and BLOCKS represent collected families of protein motifs. Thus, searching these databases entails submitting a single sequence to determine whether or not that sequence is similar to the members of an established family. Programs working in the opposite direction compare a collection of sequences with individual entries in the protein databases. An example of such a program is the Motif Search Tool, or MoST (Tatusov *et al. Proc. Natl. Acad. Sci. 91:* 12091-12095 (1994), the entirety of which is herein incorporated by reference). On the basis of an aligned set of input sequences, a weight matrix is calculated by using one of four methods (selected by the user). A weight matrix is simply a representation, position by position of how likely a particular amino acid will appear. The calculated weight matrix is then used to search the databases. To increase sensitivity, newly found sequences are added to the original data set, the weight matrix is recalculated, and the search is performed again. This procedure continues until no new sequences are found.

SUMMARY OF THE INVENTION

The present invention provides a substantially purified nucleic acid molecule that encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of: (a) glucose-6-phosphate-1-dehydrogenase; (b) 6-phosphogluconate dehydrogenase; (c) putative 6-phosphogluconate dehydrogenase; (d) D-ribulose-5-phosphate-3-epimerase; (e) ribose-5-phosphate isomerase; (f) putative ribose-5-phosphate isomerase; (g) transketolase; (h) putative transketolase; (i) transaldolase; (j) putative transaldolase; and (k) phosphoglucoisomerase.

The present invention also provides a substantially purified nucleic acid molecule that encodes a plant phosphogluconate pathway enzyme or fragment thereof, wherein the nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule

that encodes a maize putative transaldolase enzyme or fragment thereof; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

The present invention also provides a substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of (a) glucose-6-phosphate-1-dehydrogenase or fragment thereof; (b) 6-phosphogluconate dehydrogenase or fragment thereof; (c) putative 6-phosphogluconate dehydrogenase or fragment thereof; (d) D-ribulose-5-phosphate-3-epimerase or fragment thereof; (e) ribose-5-phosphate isomerase or fragment thereof; (f) putative ribose-5-phosphate isomerase or fragment thereof; (g) transketolase or fragment thereof; (h) putative transketolase or fragment thereof; (i) transaldolase or fragment thereof; (j) putative transaldolase or fragment thereof; and (k) phosphoglucoisomerase or fragment thereof.

The present invention also provides a substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 699.

The present invention also provides a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

The present invention also provides a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

The present invention also provides a substantially purified maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103.

The present invention also provides a substantially purified maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 12 through SEQ ID NO:21 and SEQ ID NO: 22 through SEQ ID NO: 103.

The present invention also provides a substantially purified putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence of a complement of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

The present invention also provides a substantially purified putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

The present invention also provides a substantially purified maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

The present invention also provides a substantially purified maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

The present invention also provides a substantially purified maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

The present invention also provides a substantially purified maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

The present invention also provides a substantially purified putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a

complement of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

The present invention also provides a substantially purified putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

The present invention also provides a substantially purified maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified maize or soybean transketolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified putative maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified putative maize or soybean transketolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the

group consisting of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified maize or soybean transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

The present invention also provides a substantially purified maize or soybean transaldolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

The present invention also provides a substantially purified putative maize transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 618.

The present invention also provides a substantially purified putative maize transaldolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 618.

The present invention also provides a substantially purified maize or soybean phosphoglucoisomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

The present invention also provides a substantially purified maize or soybean phosphoglucoisomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

The present invention also provides a purified antibody or fragment thereof which is capable of specifically binding to a maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence consisting of a complement of SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid

molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence consisting of a complement of SEQ ID NO: 618.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean phosphoglucoisomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of (a) a nucleic acid sequence which encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; (b) a nucleic acid sequence which encodes for a 6-phosphogluconate dehydrogenase enzyme or fragment thereof; (c) a nucleic acid sequence which encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; (d) a nucleic acid sequence which encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; (e) a nucleic acid sequence which encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof; (f) a nucleic acid sequence which encodes for a putative ribose-5-phosphate isomerase enzyme or fragment thereof; (g) a nucleic acid sequence which encodes for a transketolase enzyme or fragment thereof; (h) a

nucleic acid sequence which encodes for a putative transketolase enzyme or fragment thereof; (i) a nucleic acid sequence which encodes for a transaldolase enzyme or fragment thereof; (j) a nucleic acid sequence which encodes for a putative transaldolase enzyme or fragment thereof; (k) a nucleic acid sequence which encodes for a phosphoglucoisomerase enzyme or fragment thereof and (l) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (k); and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule encodes a plant phosphogluconate pathway enzyme or fragment thereof, the structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes for a 6-phosphogluconate dehydrogenase enzyme

or fragment thereof; a nucleic acid molecule that encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes for a putative ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes for a transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a putative transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a putative transaldolase enzyme or fragment thereof; and a nucleic acid molecule that encodes for a phosphoglucoisomerase enzyme or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to: (B) a transcribed nucleic acid molecule

with a transcribed strand and a non-transcribed strand, wherein a transcribed mRNA of the transcribed strand is complementary to an endogenous mRNA molecule having a nucleic acid sequence selected from the group consisting of an endogenous mRNA molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize transaldolase enzyme or fragment thereof; and an endogenous mRNA molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue comprising: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the

marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either, with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of the plant phosphogluconate pathway enzyme; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the plant phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue comprising: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule comprising a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean putative 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a

nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either; with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of the plant phosphogluconate pathway enzyme; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the plant phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue under evaluation which comprises assaying the concentration of a molecule, whose concentration is dependent upon the expression of a gene, the gene specifically hybridizes to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof, in comparison to the concentration of that molecule present in a reference plant cell or a reference plant tissue with a known level or pattern of the plant phosphogluconate pathway enzyme, wherein the assayed concentration of the molecule is compared to the assayed

concentration of the molecule in the reference plant cell or reference plant tissue with the known level or pattern of the plant phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue under evaluation which comprises assaying the concentration of a molecule, whose concentration is dependent upon the expression of a gene, the gene specifically hybridizes to a nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof; in comparison to the concentration of that molecule present in a reference plant cell or a reference plant tissue with a known level or pattern of the plant phosphogluconate pathway enzyme, wherein the assayed concentration of the molecule is compared to the assayed concentration of

the molecule in the reference plant cell or the reference plant tissue with the known level or pattern of the plant phosphogluconate pathway enzyme.

The present invention provides a method of determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid, the marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the protein in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method for determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern of a plant phosphogluconate pathway enzyme comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule comprising a nucleic acid molecule that is linked to a gene, the gene specifically hybridizes to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid

molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the plant phosphogluconate pathway enzyme in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method for determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern of a plant phosphogluconate pathway enzyme comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule comprising a nucleic acid molecule that is linked to a gene, the gene specifically hybridizes to a nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement

thereof; a nucleic acid molecule that encodes a putative maize or soybean transaldolase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof; and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the plant phosphogluconate pathway enzyme in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region has a nucleic acid sequence selected from group consisting of SEQ ID NO: 1 through SEQ ID NO: 699; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing an overexpressed plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the

structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing an overexpressed plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme

or fragment thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced levels of a plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced levels of a plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a

maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a plant phosphogluconate pathway enzyme in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1

through SEQ ID NO: 699 or complements thereof or fragments of either and the transcribed strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a plant phosphogluconate pathway enzyme in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein a transcribed mRNA of the transcribed strand is complementary to a nucleic acid molecule selected from the group consisting of an endogenous mRNA molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes

a maize or soybean transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule has a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or

fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of isolating a nucleic acid that encodes a plant phosphogluconate pathway enzyme or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either with a complementary second nucleic acid molecule obtained from a plant cell or plant tissue; (B) permitting hybridization between the first nucleic acid molecule and the second nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

The present invention also provides a method of isolating a nucleic acid molecule that encodes a plant phosphogluconate pathway enzyme or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a

nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either; with a complementary second nucleic acid molecule obtained from a plant cell or plant tissue; (B) permitting hybridization between the plant phosphogluconate pathway enzyme nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

DETAILED DESCRIPTION OF THE INVENTION

Definitions and Agents of the Present Invention

Definitions:

As used herein, a phosphogluconate pathway enzyme is any enzyme that is associated with the synthesis, oxidation, hydrolysis, or modification of phosphogluconate compounds.

As used herein, a phosphogluconate synthesis enzyme is any enzyme that is associated with the synthesis of phosphogluconate.

As used herein, a phosphogluconate oxidation enzyme is any enzyme that is associated with the oxidation of phosphogluconate.

As used herein, a phosphogluconate hydrolysis enzyme is any enzyme that is associated with the hydrolysis of phosphogluconate.

As used herein, a phosphogluconate modification enzyme is any enzyme that is associated with the modification of phosphogluconate compounds.

As used herein, glucose-6-phosphate dehydrogenase is any enzyme that catalyzes the conversion of glucose-6-phosphate to 6-phosphoglyconolactone.

As used herein, 6-phosphogluconate dehydrogenase is any enzyme that catalyzes the conversion of 6-phosphogluconate to ribulose-5-phosphate.

As used herein, ribose-5-phosphate isomerase is any enzyme that catalyzes the conversion of ribulose-5-phosphate to ribose-5-phosphate.

As used herein, ribulose-5-phosphate-3-epimerase is any enzyme that catalyzes the conversion of ribulose-5-phosphate to xylulose-5-phosphate.

As used herein, transketolase is any enzyme that catalyzes the conversion of ribose-5-phosphate and xylulose-5-phosphate to sedheptulose-7-phosphate and 3-phosphoglyceraldehyde.

As used herein, transaldolase is any enzyme that catalyzes the conversion of sedheptulose-7-phosphate and 3-phosphoglyceraldehyde to erythrose-4-phosphate and fructose-6-phosphate.

As used herein, phosphohexose isomerase (phsophoglucoisomerase) is any enzyme that catalyzes the conversion of fructose-6-phosphate to glucose-6-phosphate.

Agents

(a) Nucleic Acid Molecules

Agents of the present invention include plant nucleic acid molecules and more preferably include maize and soybean nucleic acid molecules and more preferably include nucleic acid molecules of the maize genotypes B73 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), B73 x Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), DK604 (Dekalb Genetics, Dekalb, Illinois U.S.A.), H99 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), RX601 (Asgrow Seed Company, Des Moines, Iowa), Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), and soybean types Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa), C1944 (United States Department of Agriculture (USDA) Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), FT108 (Monsoy, Brazil), Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), BW211S Null (Tohoku University, Morioka, Japan), PI507354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Asgrow A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.), PI227687 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and Asgrow A3237 (Asgrow Seed Company, Des Moines, Iowa U.S.A.).

A subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that are marker molecules. Another subset of the nucleic acid molecules of the present invention include nucleic acid molecules that encode a protein or fragment thereof. Another subset of the nucleic acid molecules of the present invention are EST molecules.

Fragment nucleic acid molecules may encode significant portion(s) of, or indeed most of, these nucleic acid molecules. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 250 nucleotide residues and more preferably, about 15 to about 30 nucleotide residues).

The term "substantially purified", as used herein, refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic and thus involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (e.g. DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (e.g. fluorescent labels, Prober *et al.*, *Science 238*:336-340 (1987); Albarella *et al.*, EP 144914; chemical labels, Sheldon *et al.*, U.S. Patent No. 4,582,789; Albarella *et al.*, U.S. Patent No. 4,563,417; modified bases, Miyoshi *et al.*, EP 119448, all of which are hereby incorporated by reference in their entirety).

It is further understood, that the present invention provides recombinant bacterial, mammalian, microbial, insect, fungal and plant cells and viral constructs comprising the agents of the present invention. (See, for example, Uses of the Agents of the Invention, Section (a) Plant Constructs and Plant Transformants; Section (b) Fungal Constructs and Fungal Transformants; Section (c) Mammalian Constructs and Transformed Mammalian Cells; Section (d) Insect Constructs and Transformed Insect Cells; and Section (e) Bacterial Constructs and Transformed Bacterial Cells)

Nucleic acid molecules or fragments thereof of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another

with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning,* A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989) and by Haymes *et al., Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985), the entirety of which is herein incorporated by reference. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

In a preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof under moderately stringent conditions, for example at about 2.0 X SSC and about 65°C.

In a particularly preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof under high stringency conditions such as 0.2 X SSC and about 65°C.

In one aspect of the present invention, the nucleic acid molecules of the present invention have one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof.

In a further more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention exhibit 100% sequence identity with a nucleic acid molecule present within MONN01, SATMON001, SATMON003 through SATMON014, SATMON016, SATMON017, SATMON019 through SATMON031, SATMON033,

SATMON034, SATMONN01, SATMONN04 through SATMONN06, LIB36, LIB83 through LIB84, CMz029 through CMz031, CMz033 through CMz037, CMz039 through CMz042, CMz044 through CMz045, CMz047 through CMz050, SOYMON001 through SOYMON038, Soy51 through Soy56, Soy58 through Soy62, Soy65 through Soy77, LIB3054, LIB3087, and LIB3094 (Monsanto Company, St. Louis, Missouri U.S.A.).

(i) Nucleic Acid Molecules Encoding Proteins or Fragments Thereof

Nucleic acid molecules of the present invention can comprise sequences that encode a phosphogluconate pathway enzyme or fragment thereof. Such phosphogluconate pathway enzymes or fragments thereof include homologues of known phosphogluconate pathway enzymes in other organisms.

In a preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of another plant phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of a fungal phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of a bacterial phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of a maize phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize phosphogluconate pathway enzyme homologue or fragment thereof of the present invention is a homologue of a soybean phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate

pathway enzyme homologue or fragment thereof of the present invention is a homologue of an *Arabidopsis thaliana* phosphogluconate pathway enzyme.

In a preferred embodiment of the present invention, the nucleic molecule of the present invention encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof where a maize or soybean phosphogluconate pathway enzyme exhibits a BLAST probability score of greater than 1E-12, preferably a BLAST probability score of between about 1E-30 and about 1E-12, even more preferably a BLAST probability score of greater than 1E-30 with its homologue.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof exhibits a % identity with its homologue of between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90% and even more preferably between about 90% and 99%. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragments thereof exhibits a % identity with its homologue of 100%.

In a preferred embodiment of the present invention, the nucleic molecule of the present invention encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof where a maize or soybean phosphogluconate pathway enzyme exhibits a BLAST score of greater than 120, preferably a BLAST score of between about 1450 and about 120, even more preferably a BLAST score of greater than 1450 with its homologue.

Nucleic acid molecules of the present invention also include non-maize, non-soybean homologues. Preferred non-maize, non-soybean homologues are selected from the group consisting of alfalfa, *Arabidopsis,* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat,

oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ ID NO: 699 or complements and fragments of either can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the entirety of which is herein incorporated by reference).

In an aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 699 due to the degeneracy in the genetic code in that they encode the same phosphogluconate pathway enzyme but differ in nucleic acid sequence.

In another further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 699 due to fact that the different nucleic acid sequence encodes a phosphogluconate pathway enzyme having one or more conservative amino acid residue. Examples of conservative substitutions are set forth in Table 1. It is understood that codons capable of coding for such conservative substitutions are known in the art.

Table 1

Original Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Cys	Ser; Ala
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof due to the fact that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

Agents of the present invention include nucleic acid molecules that encode a maize or soybean phosphogluconate pathway enzyme or fragment thereof and particularly substantially purified nucleic acid molecules selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transkealdolase enzyme or fragment thereof a nucleic acid molecule that encodes a putative maize transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Non-limiting examples of such nucleic acid molecules of the present invention are nucleic acid molecules comprising: SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof that encode for a plant phosphogluconate pathway enzyme or fragment thereof, SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11 or fragment thereof that encodes for a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103 or fragment thereof that encodes for a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214 or fragment thereof that encodes for a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299 or fragment thereof that encodes for a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311 or fragment thereof that encodes for a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318 or fragment thereof that encodes for a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437 or fragment thereof that encodes for a maize or soybean transketolase enzyme or fragment thereof; SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453 or fragment thereof that encodes for a putative maize or soybean transketolase enzyme or fragment thereof; SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617 or fragment thereof that encodes for a maize or soybean transaldolase enzyme or fragment thereof; SEQ ID NO: 618 or fragment thereof that

encodes for a putative maize transaldolase enzyme or fragment thereof; and SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699 or fragment thereof that encodes for a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

A nucleic acid molecule of the present invention can also encode an homologue of a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a maize or soybean transketolase enzyme or fragment thereof; a putative maize or soybean transketolase enzyme or fragment thereof; a maize or soybean transaldolase enzyme or fragment thereof; a putative maize transaldolase enzyme or fragment thereof; and a maize or soybean phosphoglucoisomerase enzyme or fragment thereof. As used herein a homologue protein molecule or fragment thereof is a counterpart protein molecule or fragment thereof in a second species (*e.g.*, maize copalyl diphosphate synthase is a homologue of *Arabidopsis* copalyl diphosphate synthase).

(ii) Nucleic Acid Molecule Markers and Probes

One aspect of the present invention concerns markers that include nucleic acid molecules SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either that can act as markers or other nucleic acid molecules of the present invention that can act as markers. Genetic markers of the present invention include "dominant" or "codominant" markers "Codominant markers" reveal the presence of two or more alleles (two per diploid individual) at a locus. "Dominant markers" reveal the presence of only a single allele per locus. The presence

of the dominant marker phenotype (e.g., a band of DNA) is an indication that one allele is present in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (e.g. absence of a DNA band) is merely evidence that "some other" undefined allele is present. In the case of populations where individuals are predominantly homozygous and loci are predominately dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multi-allelic, codominant markers often become more informative of the genotype than dominant markers. Marker molecules can be, for example, capable of detecting polymorphisms such as single nucleotide polymorphisms (SNPs).

SNPs are single base changes in genomic DNA sequence. They occur at greater frequency and are spaced with a greater uniformly throughout a genome than other reported forms of polymorphism. The greater frequency and uniformity of SNPs means that there is greater probability that such a polymorphism will be found near or in a genetic locus of interest than would be the case for other polymorphisms. SNPs are located in protein-coding regions and noncoding regions of a genome. Some of these SNPs may result in defective or variant protein expression (e.g., as a results of mutations or defective splicing). Analysis (genotyping) of characterized SNPs can require only a plus/minus assay rather than a lengthy measurement, permitting easier automation.

SNPs can be characterized using any of a variety of methods. Such methods include the direct or indirect sequencing of the site, the use of restriction enzymes (Botstein *et al.*, *Am. J. Hum. Genet. 32*:314-331 (1980), the entirety of which is herein incorporated reference; Konieczny and Ausubel, *Plant J. 4*:403-410 (1993), the entirety of which is herein incorporated by reference), enzymatic and chemical mismatch assays (Myers *et al.*, *Nature 313*:495-498

(1985), the entirety of which is herein incorporated by reference), allele-specific PCR (Newton *et al.*, *Nucl. Acids Res. 17*:2503-2516 (1989), the entirety of which is herein incorporated by reference; Wu *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:2757-2760 (1989), the entirety of which is herein incorporated by reference), ligase chain reaction (Barany, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:189-193 (1991), the entirety of which is herein incorporated by reference), single-strand conformation polymorphism analysis (Labrune *et al.*, *Am. J. Hum. Genet. 48*: 1115-1120 (1991), the entirety of which is herein incorporated by reference), primer-directed nucleotide incorporation assays (Kuppuswami *et al.*, *Proc. Natl. Acad. Sci. USA 88*:1143-1147 (1991), the entirety of which is herein incorporated by reference), dideoxy fingerprinting (Sarkar *et al.*, *Genomics 13*:441-443 (1992), the entirety of which is herein incorporated by reference), solid-phase ELISA-based oligonucleotide ligation assays (Nikiforov *et al.*, *Nucl. Acids Res. 22*:4167-4175 (1994), the entirety of which is herein incorporated by reference), oligonucleotide fluorescence-quenching assays (Livak *et al.*, *PCR Methods Appl. 4*:357-362 (1995), the entirety of which is herein incorporated by reference), 5'-nuclease allele-specific hybridization TaqMan assay (Livak *et al.*, *Nature Genet. 9*:341-342 (1995), the entirety of which is herein incorporated by reference), template-directed dye-terminator incorporation (TDI) assay (Chen and Kwok, *Nucl. Acids Res. 25*:347-353 (1997), the entirety of which is herein incorporated by reference), allele-specific molecular beacon assay (Tyagi *et al.*, *Nature Biotech. 16*: 49-53 (1998), the entirety of which is herein incorporated by reference), PinPoint assay (Haff and Smirnov, *Genome Res. 7*: 378-388 (1997), the entirety of which is herein incorporated by reference) and dCAPS analysis (Neff *et al.*, *Plant J. 14*:387-392 (1998), the entirety of which is herein incorporated by reference).

Additional markers, such as AFLP markers, RFLP markers and RAPD markers, can be utilized (Walton, *Seed World* 22-29 (July, 1993), the entirety of which is herein incorporated by reference; Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Paterson (ed.), CRC Press, New York (1988), the entirety of which is herein incorporated by reference). DNA markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP markers result from single base changes or insertions/deletions. These codominant markers are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction nuclease digestion but only of specific PCR products. These markers are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions.

Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant are highly abundant in genomes and exhibit a medium level of polymorphism.

SSRs require DNA sequence information. These codominant markers result from repeat length changes, are highly polymorphic and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs SNPs also require DNA sequence information. These codominant markers result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski *et al.*, In: *Nonmammalian Genomic Analysis*, Birren and

Lai (ed.), Academic Press, San Diego, CA, pp. 75-134 (1996), the entirety of which is herein incorporated by reference). It is understood that a nucleic acid molecule of the present invention may be used as a marker.

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure to with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques 25*:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

It is understood that a fragment of one or more of the nucleic acid molecules of the present invention may be a probe and specifically a PCR probe.

(b) Protein and Peptide Molecules

A class of agents comprises one or more of the protein or fragments thereof or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO: 699 or one or more of the protein or fragment thereof and peptide molecules encoded by other nucleic acid agents of the present invention. As used herein, the term “protein molecule” or “peptide molecule” includes any molecule that comprises five or more amino acids. It is well known in the art that proteins may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term “protein molecule” or “peptide molecule” includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino

acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine and homoserine.

Non-limiting examples of the protein or fragment thereof of the present invention include a maize or soybean phosphogluconate pathway enzyme or fragment thereof; a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a maize or soybean transketolase enzyme or fragment thereof; a putative maize or soybean transketolase enzyme or fragment thereof; a maize or soybean transaldolase enzyme or fragment thereof; a putative maize transaldolase enzyme or fragment thereof; and a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Non-limiting examples of the protein or fragment molecules of the present invention are a phosphogluconate pathway enzyme or fragment thereof encoded by: SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof that encode for a phosphogluconate pathway enzyme or fragment thereof, SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11 or fragment thereof that encodes for a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103 or fragment thereof that encodes for a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214 or fragment thereof that encodes for a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299 or fragment thereof that encodes for a putative maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311 or fragment thereof that encodes for a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318 or fragment thereof that encodes for a putaive maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437 or fragment thereof that encodes for a maize or soybean transketolase enzyme or fragment thereof; SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453 or fragment thereof that encodes for a putative maize or soybean transketolase enzyme or fragment thereof; SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617 or fragment thereof that encodes for a maize or a soybean transaldolase enzyme or fragment thereof; SEQ ID NO: 618 or fragment thereof that encode for a putative maize transaldolase enzyme or fragment thereof; and SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699 or fragment thereof that encodes for a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

One or more of the protein or fragment of peptide molecules may be produced via chemical synthesis, or more preferably, by expressing in a suitable bacterial or eucaryotic host. Suitable methods for expression are described by Sambrook *et al.*, (In: *Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Press*, Cold Spring Harbor, New York (1989)), or similar texts. For example, the protein may be expressed in, for example, Uses of the Agents of the Invention, Section (a) Plant Constructs and Plant Transformants; Section (b)

Fungal Constructs and Fungal Transformants; Section (c) Mammalian Constructs and Transformed Mammalian Cells; Section (d) Insect Constructs and Transformed Insect Cells; and Section (e) Bacterial Constructs and Transformed Bacterial Cells.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprise protein or peptide molecules or fragments or fusions thereof encoded by SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof in which conservative, non-essential or non-relevant amino acid residues have been added, replaced or deleted. Computerized means for designing modifications in protein structure are known in the art (Dahiyat and Mayo, *Science* 278:82-87 (1997), the entirety of which is herein incorporated by reference).

The protein molecules of the present invention include plant homologue proteins. An example of such a homologue is a homologue protein of a non-maize or non-soybean plant species, that include but not limited to alfalfa, *Arabidopsis*, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus* etc. Particularly preferred non-maize or non-soybean for use for the isolation of homologs would include, *Arabidopsis,* barley, cotton, oat, oilseed rape, rice, canola, ornamentals,

sugarcane, sugarbeet, tomato, potato, wheat and turf grasses. Such a homologue can be obtained by any of a variety of methods. Most preferably, as indicated above, one or more of the disclosed sequences (SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof) will be used to define a pair of primers that may be used to isolate the homologue-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologues by recombinant means.

(c) Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologues, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the present invention if such binding is not competitively inhibited by the presence of non-related molecules.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a "fusion" molecule (i.e., a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal and may comprise intact immunoglobulins, or antigen binding portions of immunoglobulins fragments (such as (F(ab'), $F(ab')_2$), or single-chain immunoglobulins producible, for example, via recombinant means. It is understood that practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (*see*, for example, Harlow and Lane, In: *Antibodies: A Laboratory Manual,* Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for this purpose, however, equivalent strains may also be used. The animals are preferably immunized with approximately 25 μg of purified protein (or fragment thereof) that has been emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)). Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site and one subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 μg of antigen is preferably given in normal saline three weeks later. After approximately 11 days following the second injection, the mice may be bled and the blood screened for the presence of anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay (ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection of approximately 25 μg of the same protein or fragment. The splenic leukocytes from this animal may be recovered 3 days later and then permitted to fuse, most preferably, using polyethylene glycol, with cells of a suitable myeloma cell line (such as, for example, the

P3X63Ag8.653 myeloma cell line). Hybridoma cells are selected by culturing the cells under "HAT" (hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones may then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably by direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a fusion of a protein or peptide of the present invention, or conjugate of a protein or peptide of the present invention, as immunogens. Thus, for example, a group of mice can be immunized using a fusion protein emulsified in Freund's complete adjuvant (*e.g.* approximately 50 μg of antigen per immunization). At three week intervals, an identical amount of antigen is emulsified in Freund's incomplete adjuvant and used to immunize the animals. Ten days following the third immunization, serum samples are taken and evaluated for the presence of antibody. If antibody titers are too low, a fourth booster can be employed. Polysera capable of binding the protein or peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-described immunized mice are removed, disrupted and immune splenocytes are isolated over a ficoll gradient. The isolated splenocytes are fused, using polyethylene glycol with BALB/c-derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653 plasmacytoma cells. The fused cells are plated into 96 well microtiter plates and screened for hybridoma fusion cells by their capacity to grow in culture medium supplemented with hypothanthine, aminopterin and thymidine for approximately 2-3 weeks.

Hybridoma cells that arise from such incubation are preferably screened for their capacity to produce an immunoglobulin that binds to a protein of interest. An indirect ELISA may be used for this purpose. In brief, the supernatants of hybridomas are incubated in microtiter wells

that contain immobilized protein. After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase. After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate). Such screening is performed as quickly as possible after the identification of the hybridoma in order to ensure that a desired clone is not overgrown by non-secreting neighbor cells. Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary. In a preferred sub-embodiment, a different antigenic form may be used to screen the hybridoma. Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen. It is understood that any of the protein or peptide molecules of the present invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for diagnostic purposes. Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the present invention permits the identification of mimetic compounds of those molecules. A "mimetic compound" is a compound that is not that compound, or a fragment of that compound, but which nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

It is understood that any of the agents of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Uses of the Agents of the Invention

Nucleic acid molecules and fragments thereof of the present invention may be employed to obtain other nucleic acid molecules from the same species (e.g., ESTs or fragment thereof from maize may be utilized to obtain other nucleic acid molecules from maize). Such nucleic acid molecules include the nucleic acid molecules that encode the complete coding sequence of a protein and promoters and flanking sequences of such molecules. In addition, such nucleic acid molecules include nucleic acid molecules that encode for other isozymes or gene family members. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from maize or soybean. Methods for forming such libraries are well known in the art.

Nucleic acid molecules and fragments thereof of the present invention may also be employed to obtain nucleic acid homologues. Such homologues include the nucleic acid molecule of other plants or other organisms (*e.g.*, alfalfa, *Arabidopsis*, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus,* etc.) including the nucleic acid molecules that encode, in whole or in part, protein homologues of other plant species or other organisms, sequences of genetic elements such as promoters and transcriptional regulatory elements. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from such plant species. Methods for forming such libraries are well known in the art. Such homologue molecules may differ in their nucleotide sequences from those found in one or more of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof because complete complementarity is not needed for stable hybridization. The nucleic

acid molecules of the present invention therefore also include molecules that, although capable of specifically hybridizing with the nucleic acid molecules may lack "complete complementarity."

Any of a variety of methods may be used to obtain one or more of the above-described nucleic acid molecules (Zamechik *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 83*:4143-4146 (1986), the entirety of which is herein incorporated by reference; Goodchild *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:5507-5511 (1988), the entirety of which is herein incorporated by reference; Wickstrom *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:1028-1032 (1988), the entirety of which is herein incorporated by reference; Holt *et al.*, *Molec. Cell. Biol. 8*:963-973 (1988), the entirety of which is herein incorporated by reference; Gerwirtz *et al.*, *Science 242*:1303-1306 (1988), the entirety of which is herein incorporated by reference; Anfossi *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:3379-3383 (1989), the entirety of which is herein incorporated by reference; Becker *et al.*, *EMBO J. 8*:3685-3691 (1989); the entirety of which is herein incorporated by reference). Automated nucleic acid synthesizers may be employed for this purpose. In lieu of such synthesis, the disclosed nucleic acid molecules may be used to define a pair of primers that can be used with the polymerase chain reaction (Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich *et al.*, European Patent 50,424; European Patent 84,796; European Patent 258,017; European Patent 237,362; Mullis, European Patent 201,184; Mullis *et al.*, U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki *et al.*, U.S. Patent No. 4,683,194, all of which are herein incorporated by reference in their entirety) to amplify and obtain any desired nucleic acid molecule or fragment.

Promoter sequence(s) and other genetic elements, including but not limited to transcriptional regulatory flanking sequences, associated with one or more of the disclosed nucleic acid sequences can also be obtained using the disclosed nucleic acid sequence provided

herein. In one embodiment, such sequences are obtained by incubating EST nucleic acid molecules or preferably fragments thereof with members of genomic libraries (*e.g.* maize and soybean) and recovering clones that hybridize to the EST nucleic acid molecule or fragment thereof. In a second embodiment, methods of "chromosome walking," or inverse PCR may be used to obtain such sequences (Frohman *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:8998-9002 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:5673-5677 (1989); Pang *et al.*, *Biotechniques 22:*1046-1048 (1977); Huang *et al., Methods Mol. Biol. 69:*89-96 (1997); Huang *et al., Method Mol. Biol. 67:*287-294 (1997); Benkel *et al., Genet. Anal. 13:*123-127 (1996); Hartl *et al., Methods Mol. Biol. 58:*293-301 (1996), all of which are herein incorporated by reference in their entirety).

The nucleic acid molecules of the present invention may be used to isolate promoters of cell enhanced, cell specific, tissue enhanced, tissue specific, developmentally or environmentally regulated expression profiles. Isolation and functional analysis of the 5' flanking promoter sequences of these genes from genomic libraries, for example, using genomic screening methods and PCR techniques would result in the isolation of useful promoters and transcriptional regulatory elements. These methods are known to those of skill in the art and have been described (See, for example, Birren *et al.*, *Genome Analysis*: *Analyzing DNA*, 1, (1997), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., the entirety of which is herein incorporated by reference). Promoters obtained utilizing the nucleic acid molecules of the present invention could also be modified to affect their control characteristics. Examples of such modifications would include but are not limited to enhanced sequences as reported in Uses of the Agents of the Invention, Section (a) Plant Constructs and Plant Transformants. Such genetic

elements could be used to enhance gene expression of new and existing traits for crop improvements.

In one sub-aspect, such an analysis is conducted by determining the presence and/or identity of polymorphism(s) by one or more of the nucleic acid molecules of the present invention and more preferably one or more of the EST nucleic acid molecule or fragment thereof which are associated with a phenotype, or a predisposition to that phenotype.

Any of a variety of molecules can be used to identify such polymorphism(s). In one embodiment, one or more of the EST nucleic acid molecules (or a sub-fragment thereof) may be employed as a marker nucleic acid molecule to identify such polymorphism(s). Alternatively, such polymorphisms can be detected through the use of a marker nucleic acid molecule or a marker protein that is genetically linked to (i.e., a polynucleotide that co-segregates with) such polymorphism(s).

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1mb of the polymorphism(s) and more preferably within 100kb of the polymorphism(s) and most preferably within 10kb of the polymorphism(s) can be employed.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem.* *55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (i.e., the original "allele") whereas other members may have the variant sequence (i.e., the variant "allele"). In the simplest case, only one variant sequence may exist and the polymorphism is thus said to be di-allelic. In other cases, the species' population may contain multiple alleles and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent No. 5,075,217; Armour *et al., FEBS Lett. 307*:113-115 (1992); Jones *et al., Eur. J. Haematol. 39*:144-147 (1987); Horn *et al.*, PCT Patent Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent No. 5,175,082; Jeffreys *et al., Amer. J. Hum. Genet. 39*:11-24 (1986); Jeffreys *et al., Nature 316*:76-79 (1985); Gray *et al., Proc. R. Acad. Soc. Lond. 243*:241-253 (1991); Moore *et al., Genomics 10*:654-660 (1991); Jeffreys *et al., Anim. Genet. 18*:1-15 (1987); Hillel *et al., Anim. Genet. 20*:145-155 (1989); Hillel *et al., Genet. 124*:783-789 (1990), all of which are herein incorporated by reference in their entirety).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration

of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

The most preferred method of achieving such amplification employs the polymerase chain reaction ("PCR") (Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich *et al.*, European Patent Appln. 50,424; European Patent Appln. 84,796; European Patent Application 258,017; European Patent Appln. 237,362; Mullis, European Patent Appln. 201,184; Mullis *et al.*, U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki *et al.*, U.S. Patent No. 4,683,194), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

In lieu of PCR, alternative methods, such as the "Ligase Chain Reaction" ("LCR") may be used (Barany, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:189-193 (1991), the entirety of which is herein incorporated by reference). LCR uses two pairs of oligonucleotide probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependent ligase. As with PCR, the resulting products thus serve as a template in subsequent cycles and an exponential amplification of the desired sequence is obtained.

LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a polymorphic site. In one embodiment, either oligonucleotide will be designed to include the actual polymorphic site of the polymorphism. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide that is complementary to the

polymorphic site present on the oligonucleotide. Alternatively, the oligonucleotides may be selected such that they do not include the polymorphic site (see, Segev, PCT Application WO 90/01069, the entirety of which is herein incorporated by reference).

The "Oligonucleotide Ligation Assay" ("OLA") may alternatively be employed (Landegren *et al.*, *Science 241*:1077-1080 (1988), the entirety of which is herein incorporated by reference). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. OLA, like LCR, is particularly suited for the detection of point mutations. Unlike LCR, however, OLA results in "linear" rather than exponential amplification of the target sequence.

Nickerson *et al.,* have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:8923-8927 (1990), the entirety of which is herein incorporated by reference). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA. In addition to requiring multiple and separate, processing steps, one problem associated with such combinations is that they inherit all of the problems associated with PCR and OLA.

Schemes based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, are also known (Wu *et al.*, *Genomics 4*:560-569 (1989), the entirety of which is herein incorporated by reference) and may be readily adapted to the purposes of the present invention.

Other known nucleic acid amplification procedures, such as allele-specific oligomers, branched DNA technology, transcription-based amplification systems, or isothermal amplification methods may also be used to amplify and analyze such polymorphisms (Malek *et*

al., U.S. Patent No. 5,130,238; Davey *et al.*, European Patent Application 329,822; Schuster *et al.*, U.S. Patent No. 5,169,766; Miller *et al.*, PCT Patent Application WO 89/06700; Kwoh *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:1173-1177 (1989); Gingeras *et al.*, PCT Patent Application WO 88/10315; Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 89*:392-396 (1992), all of which are herein incorporated by reference in their entirety).

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in a plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet. 32*:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet. 32*:314-331 (1980); Fischer *et al.*, (PCT Application WO90/13668); Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis. SSCP is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996), the entirety of which is herein incorporated by reference); Orita *et al., Genomics 5:*874-879 (1989), the entirety of which is herein incorporated by reference). Under denaturing conditions a single

strand of DNA will adopt a conformation that is uniquely dependent on its sequence conformation. This conformation usually will be different, even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP including, but not limited to, Lee *et al., Anal. Biochem. 205:*289-293 (1992), the entirety of which is herein incorporated by reference; Suzuki *et al., Anal. Biochem. 192:*82-84 (1991), the entirety of which is herein incorporated by reference; Lo *et al., Nucleic Acids Research 20:*1005-1009 (1992), the entirety of which is herein incorporated by reference; Sarkar *et al., Genomics 13:*441-443 (1992), the entirety of which is herein incorporated by reference. It is understood that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA (Vos *et al., Nucleic Acids Res. 23*:4407-4414 (1995), the entirety of which is herein incorporated by reference). This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence.

AFLP employs basically three steps. Initially, a sample of genomic DNA is cut with restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments

in which the primer extensions match the nucleotide flanking the restriction sites. These amplified fragments are then visualized on a denaturing polyacrylamide gel.

AFLP analysis has been performed on *Salix* (Beismann *et al.*, *Mol. Ecol. 6*:989-993 (1997), the entirety of which is herein incorporated by reference), *Acinetobacter* (Janssen *et al.*, *Int. J. Syst. Bacteriol. 47*:1179-1187 (1997), the entirety of which is herein incorporated by reference), *Aeromonas popoffi* (Huys *et al.*, *Int. J. Syst. Bacteriol. 47*:1165-1171 (1997), the entirety of which is herein incorporated by reference), rice (McCouch *et al.*, *Plant Mol. Biol. 35*:89-99 (1997), the entirety of which is herein incorporated by reference; Nandi *et al.*, *Mol. Gen. Genet. 255*:1-8 (1997), the entirety of which is herein incorporated by reference; Cho *et al.*, *Genome 39*:373-378 (1996), the entirety of which is herein incorporated by reference), barley (*Hordeum vulgare*)(Simons *et al.*, *Genomics 44*:61-70 (1997), the entirety of which is herein incorporated by reference; Waugh *et al.*, *Mol. Gen. Genet. 255*:311-321 (1997), the entirety of which is herein incorporated by reference; Qi *et al.*, *Mol. Gen Genet. 254*:330-336 (1997), the entirety of which is herein incorporated by reference; Becker *et al.*, *Mol. Gen. Genet. 249*:65-73 (1995), the entirety of which is herein incorporated by reference), potato (Van der Voort *et al.*, *Mol. Gen. Genet. 255*:438-447 (1997), the entirety of which is herein incorporated by reference; Meksem *et al.*, *Mol. Gen. Genet. 249*:74-81 (1995), the entirety of which is herein incorporated by reference), *Phytophthora infestans* (Van der Lee *et al.*, *Fungal Genet. Biol. 21*:278-291 (1997), the entirety of which is herein incorporated by reference), *Bacillus anthracis* (Keim *et al.*, *J. Bacteriol. 179*:818-824 (1997), the entirety of which is herein incorporated by reference), *Astragalus cremnophylax* (Travis *et al.*, *Mol. Ecol. 5*:735-745 (1996), the entirety of which is herein incorporated by reference), *Arabidopsis* (Cnops *et al.*, *Mol. Gen. Genet. 253*:32-41 (1996), the entirety of which is herein incorporated by reference), *Escherichia coli* (Lin *et al.*, *Nucleic*

Acids Res. *24*:3649-3650 (1996), the entirety of which is herein incorporated by reference), *Aeromonas* (Huys *et al.*, *Int. J. Syst. Bacteriol.* *46*:572-580 (1996), the entirety of which is herein incorporated by reference), nematode (Folkertsma *et al.*, *Mol. Plant Microbe Interact.* *9*:47-54 (1996), the entirety of which is herein incorporated by reference), tomato (Thomas *et al.*, *Plant J.* *8*:785-794 (1995), the entirety of which is herein incorporated by reference) and human (Latorra *et al.*, *PCR Methods Appl.* *3*:351-358 (1994), the entirety of which is herein incorporated by reference). AFLP analysis has also been used for fingerprinting mRNA (Money *et al.*, *Nucleic Acids Res.* *24*:2616-2617 (1996), the entirety of which is herein incorporated by reference; Bachem *et al.*, *Plant J.* *9*:745-753 (1996), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by AFLP analysis or for fingerprinting RNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al., Nucl. Acids Res.* *18*:6531-6535 (1990), the entirety of which is herein incorporated by reference) and cleaveable amplified polymorphic sequences (CAPS) (Lyamichev *et al.*, *Science* *260*:778-783 (1993), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Through genetic mapping, a fine scale linkage map can be developed using DNA markers and, then, a genomic DNA library of large-sized fragments can be screened with molecular markers linked to the desired trait. Molecular markers are advantageous for agronomic traits that are otherwise difficult to tag, such as resistance to pathogens, insects and nematodes, tolerance to abiotic stress, quality parameters and quantitative traits such as high yield potential.

The essential requirements for marker-assisted selection in a plant breeding program are: (1) the marker(s) should co-segregate or be closely linked with the desired trait; (2) an efficient means of screening large populations for the molecular marker(s) should be available; and (3) the screening technique should have high reproducibility across laboratories and preferably be economical to use and be user-friendly.

The genetic linkage of marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics 121*:185-199 (1989) and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics 121*:185-199 (1989) and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL,* Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety). Use of Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein,

Genetics 121:185-199 (1989) the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward *et al.*, (eds.) Chapman & Hall, London, pp. 314-331 (1993), the entirety of which is herein incorporated by reference.

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use non-parametric methods (Kruglyak and Lander, *Genetics 139:*1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.), Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994), both of which is herein incorporated by reference in their entirety). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics 136*:1447-1455 (1994), the entirety of which is herein incorporated by reference and Zeng, *Genetics 136*:1457-1468 (1994) the entirety of which is herein incorporated by reference. Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen and Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), the entirety of which is herein incorporated by reference, thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics 136*:1457-1468 (1994)). These models can be extended to multi-environment experiments to analyze genotype-

environment interactions (Jansen *et al., Theo. Appl. Genet. 91*:33-37 (1995), the entirety of which is herein incorporated by reference).

Selection of an appropriate mapping populations is important to map construction. The choice of appropriate mapping population depends on the type of marker systems employed (Tanksley *et al., Molecular mapping plant chromosomes. Chromosome structure and function: Impact of new concepts,* Gustafson and Appels (eds.), Plenum Press, New York, pp 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F_2 population is the first generation of selfing after the hybrid seed is produced. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, *Measurement of Linkage in Heredity,* Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (e.g. F_3, BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (e.g. disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (e.g. F_3 or BCF_2) can be used in map

construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (i.e., maximum disequillibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually >F_5, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (i.e., about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992), the entirety of which is herein incorporated by reference). However, as the distance between markers becomes larger (i.e., loci become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (e.g., generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former) can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al., Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992)). Information obtained from backcross populations using either codominant or dominant markers is less than that obtained from F_2 populations because one,

rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (i.e. about 15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL) created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:9828-9832 (1991), the entirety of which is herein incorporated by reference). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at unlinked regions (i.e. heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

It is understood that one or more of the nucleic acid molecules of the present invention may be used as molecular markers. It is also understood that one or more of the protein molecules of the present invention may be used as molecular markers.

In accordance with this aspect of the present invention, a sample nucleic acid is obtained from plants cells or tissues. Any source of nucleic acid may be used. Preferably, the nucleic acid is genomic DNA. The nucleic acid is subjected to restriction endonuclease digestion. For

example, one or more nucleic acid molecule or fragment thereof of the present invention can be used as a probe in accordance with the above-described polymorphic methods. The polymorphism obtained in this approach can then be cloned to identify the mutation at the coding region which alters the protein's structure or regulatory region of the gene which affects its expression level.

In an aspect of the present invention, one or more of the nucleic molecules of the present invention are used to determine the level (i.e., the concentration of mRNA in a sample, etc.) in a plant (preferably maize or soybean) or pattern (i.e., the kinetics of expression, rate of decomposition, stability profile, etc.) of the expression of a protein encoded in part or whole by one or more of the nucleic acid molecule of the present invention (collectively, the "Expression Response" of a cell or tissue). As used herein, the Expression Response manifested by a cell or tissue is said to be "altered" if it differs from the Expression Response of cells or tissues of plants not exhibiting the phenotype. To determine whether an Expression Response is altered, the Expression Response manifested by the cell or tissue of the plant exhibiting the phenotype is compared with that of a similar cell or tissue sample of a plant not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of plants not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular plant may be compared with previously obtained values of normal plants. As used herein, the phenotype of the organism is any of one or more characteristics of an organism (e.g. disease resistance, pest tolerance, environmental tolerance such as tolerance to abiotic stress, male sterility, quality improvement or yield etc.). A change in genotype or phenotype may be transient or permanent. Also as used herein, a tissue sample is any sample that comprises more than one cell. In a preferred aspect, a tissue sample comprises

cells that share a common characteristic (e.g. derived from root, seed, flower, leaf, stem or pollen etc.).

In one aspect of the present invention, an evaluation can be conducted to determine whether a particular mRNA molecule is present. One or more of the nucleic acid molecules of the present invention, preferably one or more of the EST nucleic acid molecules or fragments thereof of the present invention are utilized to detect the presence or quantity of the mRNA species. Such molecules are then incubated with cell or tissue extracts of a plant under conditions sufficient to permit nucleic acid hybridization. The detection of double-stranded probe-mRNA hybrid molecules is indicative of the presence of the mRNA; the amount of such hybrid formed is proportional to the amount of mRNA. Thus, such probes may be used to ascertain the level and extent of the mRNA production in a plant's cells or tissues. Such nucleic acid hybridization may be conducted under quantitative conditions (thereby providing a numerical value of the amount of the mRNA present). Alternatively, the assay may be conducted as a qualitative assay that indicates either that the mRNA is present, or that its level exceeds a user set, predefined value.

A principle of *in situ* hybridization is that a labeled, single-stranded nucleic acid probe will hybridize to a complementary strand of cellular DNA or RNA and, under the appropriate conditions, these molecules will form a stable hybrid. When nucleic acid hybridization is combined with histological techniques, specific DNA or RNA sequences can be identified within a single cell. An advantage of *in situ* hybridization over more conventional techniques for the detection of nucleic acids is that it allows an investigator to determine the precise spatial population (Angerer *et al., Dev. Biol. 101*:477-484 (1984), the entirety of which is herein incorporated by reference; Angerer *et al., Dev. Biol. 112*:157-166 (1985), the entirety of which is

herein incorporated by reference; Dixon *et al.*, *EMBO J. 10*:1317-1324 (1991), the entirety of which is herein incorporated by reference). *In situ* hybridization may be used to measure the steady-state level of RNA accumulation. It is a sensitive technique and RNA sequences present in as few as 5-10 copies per cell can be detected (Hardin *et al.*, *J. Mol. Biol. 202*:417-431 (1989), the entirety of which is herein incorporated by reference). A number of protocols have been devised for *in situ* hybridization, each with tissue preparation, hybridization and washing conditions (Meyerowitz, *Plant Mol. Biol. Rep. 5*:242-250 (1987), the entirety of which is herein incorporated by reference; Cox and Goldberg, In: *Plant Molecular Biology: A Practical Approach,* Shaw (ed.), pp 1-35, IRL Press, Oxford (1988), the entirety of which is herein incorporated by reference; Raikhel *et al.*, *In situ RNA hybridization in plant tissues*, In: *Plant Molecular Biology Manual*, vol. B9:1-32, Kluwer Academic Publisher, Dordrecht, Belgium (1989), the entirety of which is herein incorporated by reference).

In situ hybridization also allows for the localization of proteins within a tissue or cell (Wilkinson, *In Situ Hybridization,* Oxford University Press, Oxford (1992), the entirety of which is herein incorporated by reference; Langdale, *In Situ Hybridization* In: *The Maize Handbook,* Freeling and Walbot (eds.), pp 165-179, Springer-Verlag, New York (1994), the entirety of which is herein incorporated by reference). It is understood that one or more of the molecules of the present invention, preferably one or more of the EST nucleic acid molecules or fragments thereof of the present invention or one or more of the antibodies of the present invention may be utilized to detect the level or pattern of a phosphogluconate pathway enzyme or mRNA thereof by *in situ* hybridization.

Fluorescent *in situ* hybridization allows the localization of a particular DNA sequence along a chromosome which is useful, among other uses, for gene mapping, following

chromosomes in hybrid lines or detecting chromosomes with translocations, transversions or deletions. *In situ* hybridization has been used to identify chromosomes in several plant species (Griffor *et al., Plant Mol. Biol. 17*:101-109 (1991), the entirety of which is herein incorporated by reference; Gustafson *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:1899-1902 (1990), herein incorporated by reference; Mukai and Gill, *Genome 34*:448-452 (1991), the entirety of which is herein incorporated by reference; Schwarzacher and Heslop-Harrison, *Genome 34*:317-323 (1991); Wang *et al., Jpn. J. Genet. 66*:313-316 (1991), the entirety of which is herein incorporated by reference; Parra and Windle, *Nature Genetics 5*:17-21 (1993), the entirety of which is herein incorporated by reference). It is understood that the nucleic acid molecules of the present invention may be used as probes or markers to localize sequences along a chromosome.

Another method to localize the expression of a molecule is tissue printing. Tissue printing provides a way to screen, at the same time on the same membrane many tissue sections from different plants or different developmental stages. Tissue-printing procedures utilize films designed to immobilize proteins and nucleic acids. In essence, a freshly cut section of a tissue is pressed gently onto nitrocellulose paper, nylon membrane or polyvinylidene difluoride membrane. Such membranes are commercially available (*e.g.* Millipore, Bedford, Massachusetts U.S.A.). The contents of the cut cell transfer onto the membrane and the contents and are immobilized to the membrane. The immobilized contents form a latent print that can be visualized with appropriate probes. When a plant tissue print is made on nitrocellulose paper, the cell walls leave a physical print that makes the anatomy visible without further treatment (Varner and Taylor, *Plant Physiol. 91*:31-33 (1989), the entirety of which is herein incorporated by reference).

Tissue printing on substrate films is described by Daoust, *Exp. Cell Res. 12*:203-211 (1957), the entirety of which is herein incorporated by reference, who detected amylase, protease, ribonuclease and deoxyribonuclease in animal tissues using starch, gelatin and agar films. These techniques can be applied to plant tissues (Yomo and Taylor, *Planta 112*:35-43 (1973); the entirety of which is herein incorporated by reference; Harris and Chrispeels, *Plant Physiol.* 56:292-299 (1975), the entirety of which is herein incorporated by reference). Advances in membrane technology have increased the range of applications of Daoust's tissue-printing techniques allowing (Cassab and Varner, *J. Cell. Biol. 105*:2581-2588 (1987), the entirety of which is herein incorporated by reference) the histochemical localization of various plant enzymes and deoxyribonuclease on nitrocellulose paper and nylon (Spruce *et al.*, *Phytochemistry 26:*2901-2903 (1987), the entirety of which is herein incorporated by reference; Barres *et al., Neuron 5:*527-544 (1990), the entirety of which is herein incorporated by reference; Reid and Pont-Lezica, *Tissue Printing: Tools for the Study of Anatomy, Histochemistry and Gene Expression,* Academic Press, New York, New York (1992), the entirety of which is herein incorporated by reference; Reid *et al., Plant Physiol. 93:*160-165 (1990), the entirety of which is herein incorporated by reference; Ye *et al.*, *Plant J. 1:*175-183 (1991), the entirety of which is herein incorporated by reference).

It is understood that one or more of the molecules of the present invention, preferably one or more of the EST nucleic acid molecules or fragments thereof of the present invention or one or more of the antibodies of the present invention may be utilized to detect the presence or quantity of a phosphogluconate pathway enzyme by tissue printing.

Further it is also understood that any of the nucleic acid molecules of the present invention may be used as marker nucleic acids and or probes in connection with methods that

require probes or marker nucleic acids. As used herein, a probe is an agent that is utilized to determine an attribute or feature (e.g. presence or absence, location, correlation, etc.) of a molecule, cell, tissue or plant. As used herein, a marker nucleic acid is a nucleic acid molecule that is utilized to determine an attribute or feature (*e.g.,* presence or absence, location, correlation, etc.) or a molecule, cell, tissue or plant.

A microarray-based method for high-throughput monitoring of plant gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (Schena *et al.*, *Science 270*:467-470 (1995), the entirety of which is herein incorporated by reference; Shalon, Ph.D. Thesis, Stanford University (1996), the entirety of which is herein incorporated by reference). Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several microarray methods have been described. One method compares the sequences to be analyzed by hybridization to a set of oligonucleotides representing all possible subsequences (Bains and Smith, *J. Theor. Biol. 135*:303-307 (1989), the entirety of which is herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA molecules. An array consisting of oligonucleotides complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

The microarray approach may be used with polypeptide targets (U.S. Patent No. 5,445,934; U.S. Patent No. 5,143,854; U.S. Patent No. 5,079,600; U.S. Patent No. 4,923,901, all of which are herein incorporated by reference in their entirety). Essentially, polypeptides are synthesized on a substrate (microarray) and these polypeptides can be screened with either protein molecules or fragments thereof or nucleic acid molecules in order to screen for either protein molecules or fragments thereof or nucleic acid molecules that specifically bind the target polypeptides. (Fodor *et al*., *Science 251*:767-773 (1991), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules or protein or fragments thereof of the present invention may be utilized in a microarray based method.

In a preferred embodiment of the present invention microarrays may be prepared that comprise nucleic acid molecules where such nucleic acid molecules encode at least one, preferably at least two, more preferably at least three phosphogluconate pathway enzymes, more preferably at least four phosphogluconate pathway enzymes, more preferably at least five phosphogluconate pathway enzymes, more preferably at least six phosphogluconate pathway enzymes, more preferably at least seven phosphogluconate pathway enzymes, more preferably at least eight phosphogluconate pathway enzymes, more preferably at least nine phosphogluconate pathway enzymes, more preferably at least ten phosphogluconate pathway enzymes, and even more preferably at least eleven phosphogluconate pathway enzymes.

In a preferred embodiment the nucleic acid molecules are selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid

molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or fragment thereof; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Site directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be altered (e.g. a threonine to be replaced by a methionine). Three basic methods for site directed mutagenesis are often employed. These are cassette mutagenesis (Wells *et al.*, *Gene 34*:315-323 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene 12*:129-137 (1980), the entirety of which is herein incorporated by reference; Zoller and Smith, *Methods Enzymol. 100*:468-500 (1983), the entirety of which is herein incorporated by reference; Dalbadie-McFarland *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 79*:6409-6413 (1982), the entirety of which is herein incorporated by reference) and methods based upon PCR (Scharf *et al.*, *Science 233*:1076-1078 (1986), the entirety of which is herein incorporated by reference; Higuchi *et al.*, *Nucleic Acids Res. 16*:7351-7367 (1988), the entirety of which is herein incorporated by reference). Site directed mutagenesis approaches are also

described in European Patent 0 385 962, the entirety of which is herein incorporated by reference; European Patent 0 359 472, the entirety of which is herein incorporated by reference; and PCT Patent Application WO 93/07278, the entirety of which is herein incorporated by reference.

Site directed mutagenesis strategies have been applied to plants for both *in vitro* as well as *in vivo* site directed mutagenesis (Lanz *et al.*, *J. Biol. Chem. 266*:9971-9976 (1991), the entirety of which is herein incorporated by reference; Kovgan and Zhdanov, *Biotekhnologiya 5*:148-154; No. 207160n, Chemical Abstracts 110:225 (1989), the entirety of which is herein incorporated by reference; Ge *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:4037-4041 (1989), the entirety of which is herein incorporated by reference; Zhu *et al.*, *J. Biol. Chem. 271*:18494-18498 (1996), the entirety of which is herein incorporated by reference; Chu *et al.*, *Biochemistry 33*:6150-6157 (1994), the entirety of which is herein incorporated by reference; Small *et al.*, *EMBO J. 11*:1291-1296 (1992), the entirety of which is herein incorporated by reference; Cho *et al.*, *Mol. Biotechnol. 8*:13-16 (1997), the entirety of which is herein incorporated by reference; Kita *et al.*, *J. Biol. Chem. 271*:26529-26535 (1996), the entirety of which is herein incorporated by reference, Jin *et al.*, *Mol. Microbiol. 7*:555-562 (1993), the entirety of which is herein incorporated by reference; Hatfield and Vierstra, *J. Biol. Chem. 267*:14799-14803 (1992), the entirety of which is herein incorporated by reference; Zhao *et al.*, *Biochemistry 31*:5093-5099 (1992), the entirety of which is herein incorporated by reference).

Any of the nucleic acid molecules of the present invention may either be modified by site directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners are familiar with such as

isolating restriction fragments and ligating such fragments into an expression vector (*see,* for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989)).

Sequence-specific DNA-binding proteins play a role in the regulation of transcription. The isolation of recombinant cDNAs encoding these proteins facilitates the biochemical analysis of their structural and functional properties. Genes encoding such DNA-binding proteins have been isolated using classical genetics (Vollbrecht *et al., Nature 350*: 241-243 (1991), the entirety of which is herein incorporated by reference) and molecular biochemical approaches, including the screening of recombinant cDNA libraries with antibodies (Landschulz *et al., Genes Dev. 2*:786-800 (1988), the entirety of which is herein incorporated by reference) or DNA probes (Bodner *et al., Cell 55*:505-518 (1988), the entirety of which is herein incorporated by reference). In addition, an *in situ* screening procedure has been used and has facilitated the isolation of sequence-specific DNA-binding proteins from various plant species (Gilmartin *et al., Plant Cell 4*:839-849 (1992), the entirety of which is herein incorporated by reference; Schindler *et al., EMBO J. 11*:1261-1273 (1992), the entirety of which is herein incorporated by reference). An *in situ* screening protocol does not require the purification of the protein of interest (Vinson *et al., Genes Dev. 2*:801-806 (1988), the entirety of which is herein incorporated by reference; Singh *et al., Cell 52*:415-423 (1988), the entirety of which is herein incorporated by reference).

Two steps may be employed to characterize DNA-protein interactions. The first is to identify promoter fragments that interact with DNA-binding proteins, to titrate binding activity, to determine the specificity of binding and to determine whether a given DNA-binding activity can interact with related DNA sequences (Sambrook *et al., Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York

(1989)). Electrophoretic mobility-shift assay is a widely used assay. The assay provides a rapid and sensitive method for detecting DNA-binding proteins based on the observation that the mobility of a DNA fragment through a nondenaturing, low-ionic strength polyacrylamide gel is retarded upon association with a DNA-binding protein (Fried and Crother, *Nucleic Acids Res. 9*:6505-6525 (1981), the entirety of which is herein incorporated by reference). When one or more specific binding activities have been identified, the exact sequence of the DNA bound by the protein may be determined. Several procedures for characterizing protein/DNA-binding sites are used, including methylation and ethylation interference assays (Maxam and Gilbert, *Methods Enzymol. 65*:499-560 (1980), the entirety of which is herein incorporated by reference; Wissman and Hillen, *Methods Enzymol. 208*:365-379 (1991), the entirety of which is herein incorporated by reference), footprinting techniques employing DNase I (Galas and Schmitz, *Nucleic Acids Res. 5*:3157-3170 (1978), the entirety of which is herein incorporated by reference), 1,10-phenanthroline-copper ion methods (Sigman *et al., Methods Enzymol. 208*:414-433 (1991), the entirety of which is herein incorporated by reference) and hydroxyl radicals methods (Dixon *et al., Methods Enzymol. 208*:414-433 (1991), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention may be utilized to identify a protein or fragment thereof that specifically binds to a nucleic acid molecule of the present invention. It is also understood that one or more of the protein molecules or fragments thereof of the present invention may be utilized to identify a nucleic acid molecule that specifically binds to it.

A two-hybrid system is based on the fact that many cellular functions are carried out by proteins, such as transcription factors, that interact (physically) with one another. Two-hybrid systems have been used to probe the function of new proteins (Chien *et al., Proc. Natl. Acad. Sci.*

(U.S.A.) 88:9578-9582 (1991) the entirety of which is herein incorporated by reference; Durfee *et al., Genes Dev. 7*:555-569 (1993) the entirety of which is herein incorporated by reference; Choi *et al., Cell 78*:499-512 (1994), the entirety of which is herein incorporated by reference; Kranz *et al., Genes Dev. 8*:313-327 (1994), the entirety of which is herein incorporated by reference).

Interaction mating techniques have facilitated a number of two-hybrid studies of protein-protein interaction. Interaction mating has been used to examine interactions between small sets of tens of proteins (Finley and Brent, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:12098-12984 (1994), the entirety of which is herein incorporated by reference), larger sets of hundreds of proteins (Bendixen *et al., Nucl. Acids Res. 22*:1778-1779 (1994), the entirety of which is herein incorporated by reference) and to comprehensively map proteins encoded by a small genome (Bartel *et al., Nature Genetics 12*:72-77 (1996), the entirety of which is herein incorporated by reference). This technique utilizes proteins fused to the DNA-binding domain and proteins fused to the activation domain. They are expressed in two different haploid yeast strains of opposite mating type and the strains are mated to determine if the two proteins interact. Mating occurs when haploid yeast strains come into contact and result in the fusion of the two haploids into a diploid yeast strain. An interaction can be determined by the activation of a two-hybrid reporter gene in the diploid strain. An advantage of this technique is that it reduces the number of yeast transformations needed to test individual interactions. It is understood that the protein-protein interactions of protein or fragments thereof of the present invention may be investigated using the two-hybrid system and that any of the nucleic acid molecules of the present invention that encode such proteins or fragments thereof may be used to transform yeast in the two-hybrid system.

(a) Plant Constructs and Plant Transformants

One or more of the nucleic acid molecules of the present invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. Such genetic material may be transferred into either monocotyledons and dicotyledons including, but not limited to maize (pp 63-69), soybean (pp 50-60), *Arabidopsis* (p 45), phaseolus (pp 47-49), peanut (pp 49-50), alfalfa (p 60), wheat (pp 69-71), rice (pp 72-79), oat (pp 80-81), sorghum (p 83), rye (p 84), tritordeum (p 84), millet (p85), fescue (p 85), perennial ryegrass (p 86), sugarcane (p87), cranberry (p101), papaya (pp 101-102), banana (p 103), banana (p 103), muskmelon (p 104), apple (p 104), cucumber (p 105), dendrobium (p 109), gladiolus (p 110), chrysanthemum (p 110), liliacea (p 111), cotton (pp113-114), eucalyptus (p 115), sunflower (p 118), canola (p 118), turfgrass (p121), sugarbeet (p 122), coffee (p 122) and dioscorea (p 122) (Christou, In: *Particle Bombardment for Genetic Engineering of Plants,* Biotechnology Intelligence Unit. Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a transformed cell or transformed plant. Particularly, any of the phosphogluconate pathway enzymes or fragments thereof may be overexpressed in a transformed cell or transgenic plant. Such overexpression may be the result of transient or stable transfer of the exogenous genetic material.

Exogenous genetic material may be transferred into a plant cell and the plant cell by the use of a DNA vector or construct designed for such a purpose. Design of such a vector is generally within the skill of the art (*See*, *Plant Molecular Biology: A Laboratory Manual*, Clark (ed.), Springier, New York (1997), the entirety of which is herein incorporated by reference).

A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:5745-5749 (1987), the entirety of which is herein incorporated by reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al.*, *Plant Mol. Biol. 9*:315-324 (1987), the entirety of which is herein incorporated by reference) and the CAMV 35S promoter (Odell *et al.*, *Nature 313*:810-812 (1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter (Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase promoter (Yang *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:4144-4148 (1990), the entirety of which is herein incorporated by reference), the R gene complex promoter (Chandler *et al.*, *The Plant Cell 1*:1175-1183 (1989), the entirety of which is herein incorporated by reference) and the chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs which have been expressed in plants; *see*, *e.g.*, PCT publication WO 84/02913, herein incorporated by reference in its entirety.

Promoters which are known or are found to cause transcription of DNA in plant cells can be used in the present invention. Such promoters may be obtained from a variety of sources such as plants and plant viruses. It is preferred that the particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of the phosphogluconate pathway enzyme to cause the desired phenotype. In addition to promoters that are known to cause transcription of DNA in plant cells, other promoters may be identified for use in the current invention by screening a plant cDNA library for genes which are selectively or preferably expressed in the target tissues or cells.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:3459-3463 (1990), herein incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet. 225*:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J. 8*:2445-2451 (1989), herein incorporated by reference in its entirety), the serine/threonine kinase (PAL) promoter and the glucoamylase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol. 35*:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the Cab-1 gene from wheat (Fejes *et*

al., *Plant Mol. Biol.* *15*:921-932 (1990), herein incorporated by reference in its entirety), the promoter for the CAB-1 gene from spinach (Lubberstedt *et al.*, *Plant Physiol.* *104*:997-1006 (1994), herein incorporated by reference in its entirety), the promoter for the cab1R gene from rice (Luan *et al.*, *Plant Cell.* *4*:971-981 (1992), the entirety of which is herein incorporated by reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from maize (Matsuoka *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 90*: 9586-9590 (1993), herein incorporated by reference in its entirety), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al.*, *Plant Mol. Biol.* *33*:245-255 (1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.*, *Planta.* *196*:564-570 (1995), herein incorporated by reference in its entirety) and the promoter for the thylakoid membrane proteins from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the present invention, such as the promoters for LhcB gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol.* *28*:219-229 (1995), the entirety of which is herein incorporated by reference).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of maize, wheat, rice and barley, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including the class I patatin promoter (Bevan *et al.*, *EMBO J.* *8*:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol.* *14*:995-1006 (1990), both of which are herein incorporated by reference in its entirety), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene.* *60*:47-56 (1987), Salanoubat and Belliard, *Gene.* *84*:181-185 (1989), both of which are incorporated by reference

in their entirety), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol. 101*:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol. 17*:691-699 (1991), herein incorporated by reference in its entirety) and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol Gen Genet. 219*:390-396 (1989); Mignery *et al.*, *Gene. 62*:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a phosphogluconate pathway enzyme or fragment thereof in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*: 112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in maize endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982), herein incorporated by reference in its entirety) and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD and γ genes, could also be used. Other promoters known to function, for example, in maize include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins and sucrose synthases. A particularly preferred promoter for maize endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al.*, *Mol. Cell Biol. 13*:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrosynthase (ADPGPP) subunits, the granule bound and other starch synthase, the branching and debranching enzymes,

the embryogenesis-abundant proteins, the gliadins and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al.*, *Plant Mol. Biol. 25*:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those reported by Conkling *et al.* (Conkling *et al.*, *Plant Physiol. 93*:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435; and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell 1*:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include with the coding region of interest a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the NOS 3' sequence

(Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983), the entirety of which is herein incorporated by reference), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil *et al.*, Plant Physiol. 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene (Potrykus *et al.*, *Mol. Gen. Genet. 199*:183-188 (1985), the entirety of which is herein incorporated by reference) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology 6*:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem. 263*:6310-6314 (1988), the entirety of which is herein incorporated by reference); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem. 263*:12500-12508 (1988), the entirety of which is herein incorporated by reference).

A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al., Plant Mol. Biol. 32*:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β-glucuronidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol, Rep. 5*:387-405 (1987), the entirety of which is herein incorporated by reference; Jefferson *et al., EMBO J. 6*:3901-3907 (1987), the entirety of which is herein incorporated by reference); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, Stadler Symposium *11*:263-282 (1988), the entirety of which is herein incorporated by reference); a β-lactamase gene (Sutcliffe *et al., Proc. Natl. Acad. Sci. (U.S.A.) 75*:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a

luciferase gene (Ow *et al.*, *Science 234*:856-859 (1986), the entirety of which is herein incorporated by reference); a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 80*:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a catechol diozygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*, *Bio/Technol. 8*:241-242 (1990), the entirety of which is herein incorporated by reference); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol. 129*:2703-2714 (1983), the entirety of which is herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which will turn a chromogenic α-galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins which are detectable, (*e.g.*, by ELISA), small active enzymes which are detectable in extracellular solution (*e.g.*, α-amylase, β-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of

nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc (Potrykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol. 42*:205-225 (1991), the entirety of which is herein incorporated by reference; Vasil, *Plant Mol. Biol. 25*:925-937 (1994), the entirety of which is herein incorporated by reference). For example, electroporation has been used to transform maize protoplasts (Fromm *et al.*, *Nature 312*:791-793 (1986), the entirety of which is herein incorporated by reference).

Other vector systems suitable for introducing transforming DNA into a host plant cell include but are not limited to binary artificial chromosome (BIBAC) vectors (Hamilton *et al., Gene 200*:107-116 (1997), the entirety of which is herein incorporated by reference); and transfection with RNA viral vectors (Della-Cioppa *et al., Ann. N.Y. Acad. Sci.* (1996), 792 (Engineering Plants for Commercial Products and Applications), 57-61, the entirety of which is herein incorporated by reference). Additional vector systems also include plant selectable YAC vectors such as those described in Mullen *et al.*, *Molecular Breeding 4*:449-457 (1988), the entireity of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology* 54:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell* 22:479-488 (1980), the entirety of which is herein incorporated by reference), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun. 107*:584-587 (1982); Fromm *et al., Proc. Natl. Acad. Sci. (U.S.A.) 82*:5824-5828 (1985); U.S. Patent No. 5,384,253, all of which are herein incorporated in their entirety); and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-

365 (1994), the entirety of which is herein incorporated by reference); (3) viral vectors (Clapp, *Clin. Perinatol. 20*:155-168 (1993); Lu *et al., J. Exp. Med. 178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques 6*:608-614 (1988), all of which are herein incorporated in their entirety); and (4) receptor-mediated mechanisms (Curiel *et al., Hum. Gen. Ther. 3*:147-154 (1992), Wagner *et al., Proc. Natl. Acad. Sci. (USA) 89*:6099-6103 (1992), both of which are incorporated by reference in their entirety).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou (eds.), *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly transforming monocots, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol. 87*:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection are required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics α-particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.,* describes the basic procedure for coating

tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell 2*:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-1000/He gun is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique 3*:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the pre-bombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately

after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include the particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:8526-8530 (1990); Svab and Maliga, *Proc. Natl. Acad. Sci. (U.S.A.) 90:*913-917 (1993); Staub and Maliga, *EMBO J. 12:*601-606 (1993); U.S. Patent Nos. 5, 451,513 and 5,545,818, all of which are herein incorporated by reference in their entirety).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated

plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described by Fraley *et al., Bio/Technology 3*:629-635 (1985) and Rogers *et al., Methods Enzymol. 153*:253-277 (1987), both of which are herein incorporated by reference in their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border sequences and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol. Gen. Genet. 205*:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in E. *coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.,* In: *Plant DNA Infectious Agents*, Hohn and Schell (eds.), Springer-Verlag, New York, pp. 179-203 (1985), the entirety of which is herein incorporated by reference. Moreover, technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al., Methods Enzymol. 153*:253-277 (1987)). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same

locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation and combinations of these treatments (*See, for example*, Potrykus *et al., Mol. Gen. Genet. 205*:193-200 (1986); Lorz *et al., Mol. Gen. Genet. 199*:178 (1985); Fromm *et al., Nature 319*:791 (1986); Uchimiya *et al., Mol. Gen. Genet. 204*:204 (1986); Marcotte *et al., Nature 335*:454-457 (1988), all of which are herein incorporated by reference in their entirety).

Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al., Plant Tissue Culture Letters 2*:74 (1985); Toriyama *et al., Theor Appl. Genet. 205*:34 (1986); Yamada *et al., Plant Cell Rep. 4*:85 (1986); Abdullah *et al., Biotechnolog 4*:1087 (1986), all of which are herein incorporated by reference in their entirety).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of

cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology 6*:397 (1988), the entirety of which is herein incorporated by reference). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al., Bio/Technology 10*:667 (1992), the entirety of which is herein incorporated by reference).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al., Nature 328:*70 (1987); Klein *et al., Proc. Natl. Acad. Sci. (U.S.A.) 85*:8502-8505 (1988); McCabe *et al., Bio/Technology 6:923* (1988), all of which are herein incorporated by reference in their entirety). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Zhou *et al., Methods Enzymol. 101:*433 (1983); Hess *et al., Intern Rev. Cytol. 107:*367 (1987); Luo *et al., Plant Mol Biol. Reporter 6:*165 (1988), all of which are herein incorporated by reference in their entirety), by direct injection of DNA into reproductive organs of a plant (Pena *et al., Nature 325*:274 (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of desiccated embryos (Neuhaus *et al., Theor. Appl. Genet. 75*:30 (1987), the entirety of which is herein incorporated by reference).

The regeneration, development and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, In: *Methods for Plant Molecular Biology*, Academic Press, San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process

typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens* and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863; U.S. Patent No. 5,159,135; U.S. Patent No. 5,518,908, all of which are herein incorporated by reference in their entirety); soybean (U.S. Patent No. 5,569,834; U.S. Patent No. 5,416,011; McCabe *et. al., Biotechnology 6:*923 (1988); Christou *et al., Plant Physiol. 87*:671-674 (1988); all of which are herein incorporated by reference in their entirety); *Brassica* (U.S. Patent No. 5,463,174, the entirety of which is herein incorporated by reference); peanut (Cheng *et al., Plant Cell Rep. 15:*653-657 (1996), McKently *et al., Plant Cell Rep. 14:*699-703 (1995), all of which

are herein incorporated by reference in their entirety); papaya; and pea (Grant *et al., Plant Cell Rep. 15*:254-258 (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci. (USA) 84*:5354 (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol 104:*37 (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al., Science 240:*204 (1988); Gordon-Kamm *et al., Plant Cell* 2:603-618 (1990); Fromm *et al., Bio/Technology 8*:833 (1990); Koziel *et al., Bio/Technology 11*:194 (1993); Armstrong *et al., Crop Science 35:*550-557 (1995); all of which are herein incorporated by reference in their entirety); oat (Somers *et al., Bio/Technology 10*:1589 (1992), the entirety of which is herein incorporated by reference); orchard grass (Horn *et al., Plant Cell Rep. 7*:469 (1988), the entirety of which is herein incorporated by reference); rice (Toriyama *et al., Theor Appl. Genet. 205*:34 (1986); Part *et al., Plant Mol. Biol. 32*:1135-1148 (1996); Abedinia *et al., Aust. J. Plant Physiol. 24:*133-141 (1997); Zhang and Wu, *Theor. Appl. Genet. 76*:835 (1988); Zhang *et al., Plant Cell Rep. 7*:379 (1988); Battraw and Hall, *Plant Sci. 86*:191-202 (1992); Christou *et al., Bio/Technology 9*:957 (1991), all of which are herein incorporated by reference in their entirety); rye (De la Pena *et al., Nature 325*:274 (1987), the entirety of which is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J. 2*:409 (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang *et al., Bio/Technology 10*:691 (1992), the entirety of which is herein incorporated by reference) and wheat (Vasil *et al., Bio/Technology 10*:667 (1992), the entirety of which is herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.)

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte *et al., Nature 335*:454-457 (1988), the entirety of which is herein incorporated by reference; Marcotte *et al., Plant Cell 1*:523-532 (1989), the entirety of which is herein incorporated by reference; McCarty *et al., Cell 66:*895-905 (1991), the entirety of which is herein incorporated by reference; Hattori *et al., Genes Dev. 6:*609-618 (1992), the entirety of which is herein incorporated by reference; Goff *et al., EMBO J. 9:*2517-2522 (1990), the entirety of which is herein incorporated by reference). Transient expression systems may be used to functionally dissect gene constructs (*see generally*, Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers etc. Further, any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a manner that allows for overexpression of the protein or fragment thereof encoded by the nucleic acid molecule.

Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene (Napoli *et al., Plant Cell 2*:279-289 (1990), the entirety of which is herein incorporated by reference; van der Krol *et al., Plant Cell 2*:291-299 (1990), the entirety of which is herein incorporated by reference). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the

cell (Prolls and Meyer, *Plant J. 2*:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al., Mol. Gen. Genet. 244*:325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III 316*:1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example, been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the glucoamylase (CHS) gene produced white flowers or floral sectors; this was as a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:3490-3496 (1994), the entirety of which is herein incorporated by reference); van Blokland *et al., Plant J. 6*:861-877 (1994), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene and can be reset by a developmental control mechanism (Jorgensen, *Trends Biotechnol. 8*:340-344 (1990), the entirety of which is herein incorporated by reference; Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants*, Paszkowski (ed.), pp. 335-348, Kluwer Academic, Netherlands (1994), the entirety of which is herein incorporated by reference).

It is understood that one or more of the nucleic acids of the present invention may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the cosuppression of an endogenous phosphogluconate pathway enzyme.

Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol *et al., FEBS Lett. 268*:427-430 (1990), the entirety of which is herein

incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al.,* In: *Genetic Engineering,* Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al.*, *Annu. Rev. Biochem. 55*:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol. 25*:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that the activity of a phosphogluconate pathway enzyme in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule whose non-transcribed strand encodes a phosphogluconate pathway enzyme or fragment thereof.

Antibodies have been expressed in plants (Hiatt *et al., Nature 342:*76-78 (1989), the entirety of which is herein incorporated by reference; Conrad and Fielder, *Plant Mol. Biol. 26:*1023-1030 (1994), the entirety of which is herein incorporated by reference). Cytoplamsic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips *et al., EMBO J. 16:*4489-4496 (1997), the entirety of which is herein incorporated by reference; Marion-Poll, *Trends in Plant Science 2:*447-448 (1997), the entirety of which is herein incorporated by reference). For example, expressed anti-abscisic antibodies have been reported to result in a general perturbation of seed development (Philips *et al., EMBO J. 16:* 4489-4496 (1997)).

Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, *Nature Biotechnology 15:*1313-1315 (1997), the entirety of which is herein incorporated by reference; Baca *et al., Ann. Rev. Biophys. Biomol. Struct. 26:*461-493 (1997), the entirety of which is herein incorporated by reference). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No. 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent No. 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent

No. 5,500,358; U.S. Patent No. 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the present invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

(b) Fungal Constructs and Fungal Transformants

The present invention also relates to a fungal recombinant vector comprising exogenous genetic material. The present invention also relates to a fungal cell comprising a fungal recombinant vector. The present invention also relates to methods for obtaining a recombinant fungal host cell comprising introducing into a fungal host cell exogenous genetic material.

Exogenous genetic material may be transferred into a fungal cell. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention. The fungal recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the fungal host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the fungal host.

The fungal vector may be an autonomously replicating vector, *i.e.*, a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a plasmid, an extrachromosomal element, a minichromosome, or an artificial

chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the fungal cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. For integration, the vector may rely on the nucleic acid sequence of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the fungal host. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences which individually contain a sufficient number of nucleic acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. These nucleic acid sequences may be any sequence that is homologous with a target sequence in the genome of the fungal host cell and, furthermore, may be non-encoding or encoding sequences.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of origin of replications for use in a yeast host cell are the 2 micron origin of replication and the combination of CEN3 and ARS 1. Any origin of replication may be used which is compatible with the fungal host cell of choice.

The fungal vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals,

prototrophy to auxotrophs and the like. The selectable marker may be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), hygB (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase) and *sC* (sulfate adenyltransferase) and *trpC* (anthranilate synthase). Preferred for use in an *Aspergillus* cell are the *amdS* and *pyrG* markers of *Aspergillus nidulans* or *Aspergillus oryzae* and the bar marker of *Streptomyces hygroscopicus*. Furthermore, selection may be accomplished by co-transformation, *e.g.*, as described in WO 91/17243, the entirety of which is herein incorporated by reference. A nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence which is recognized by the fungal host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the protein or fragment thereof.

A promoter may be any nucleic acid sequence which shows transcriptional activity in the fungal host cell of choice and may be obtained from genes encoding polypeptides either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of a nucleic acid construct of the invention in a filamentous fungal host are promoters obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase and hybrids thereof. In a yeast host, a useful promoter is the *Saccharomyces cerevisiae* enolase (eno-1) promoter. Particularly preferred promoters are the TAKA amylase, NA2-tpi (a hybrid of the promoters from the genes encoding

Aspergillus niger neutral alpha -amylase and *Aspergillus oryzae* triose phosphate isomerase) and glaA promoters.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a terminator sequence at its 3' terminus. The terminator sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any terminator which is functional in the fungal host cell of choice may be used in the present invention, but particularly preferred terminators are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase and *Saccharomyces cerevisiae* enolase.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the fungal host cell of choice may be used in the present invention, but particularly preferred leaders are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase and *Aspergillus oryzae* triose phosphate isomerase.

A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the fungal host to add polyadenosine residues to transcribed mRNA. The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or

fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the fungal host of choice may be used in the present invention, but particularly preferred polyadenylation sequences are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase and *Aspergillus niger* alpha-glucosidase.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and to minimize the amount of possible degradation of the expressed protein or fragment thereof within the cell, it is preferred that expression of the protein or fragment thereof gives rise to a product secreted outside the cell. To this end, a protein or fragment thereof of the present invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the fungal host into the culture medium. The signal peptide may be native to the protein or fragment thereof of the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the present invention may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to that portion of the coding sequence which encodes the secreted protein or fragment thereof. The foreign signal peptide may be required where the coding sequence does not normally contain a signal peptide coding region. Alternatively, the foreign signal peptide may simply replace the natural signal peptide to obtain enhanced secretion of the desired protein or fragment thereof. The foreign signal peptide coding region may be obtained from a glucoamylase or an amylase gene from an *Aspergillus* species, a lipase or proteinase gene

from *Rhizomucor miehei*, the gene for the alpha-factor from *Saccharomyces cerevisiae*, or the calf preprochymosin gene. An effective signal peptide for fungal host cells is the *Aspergillus oryzae* TAKA amylase signal, *Aspergillus niger* neutral amylase signal, the *Rhizomucor miehei* aspartic proteinase signal, the *Humicola lanuginosus* cellulase signal, or the *Rhizomucor miehei* lipase signal. However, any signal peptide capable of permitting secretion of the protein or fragment thereof in a fungal host of choice may be used in the present invention.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be linked to a propeptide coding region. A propeptide is an amino acid sequence found at the amino terminus of aproprotein or proenzyme. Cleavage of the propeptide from the proprotein yields a mature biochemically active protein. The resulting polypeptide is known as a propolypeptide or proenzyme (or a zymogen in some cases). Propolypeptides are generally inactive and can be converted to mature active polypeptides by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide or proenzyme. The propeptide coding region may be native to the protein or fragment thereof or may be obtained from foreign sources. The foreign propeptide coding region may be obtained from the *Saccharomyces cerevisiae* alpha-factor gene or *Myceliophthora thermophila* laccase gene (WO 95/33836, the entirety of which is herein incorporated by reference).

The procedures used to ligate the elements described above to construct the recombinant expression vector of the present invention are well known to one skilled in the art (see, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring Harbor, N.Y., (1989)).

The present invention also relates to recombinant fungal host cells produced by the methods of the present invention which are advantageously used with the recombinant vector of

the present invention. The cell is preferably transformed with a vector comprising a nucleic acid sequence of the invention followed by integration of the vector into the host chromosome. The choice of fungal host cells will to a large extent depend upon the gene encoding the protein or fragment thereof and its source. The fungal host cell may, for example, be a yeast cell or a filamentous fungal cell.

"Yeast" as used herein includes *Ascosporogenous* yeast (*Endomycetales*), *Basidiosporogenous* yeast and yeast belonging to the *Fungi Imperfecti* (*Blastomycetes*). The *Ascosporogenous* yeasts are divided into the families *Spermophthoraceae* and *Saccharomycetaceae*. The latter is comprised of four subfamilies, *Schizosaccharomycoideae* (for example, genus *Schizosaccharomyces*), *Nadsonioideae, Lipomycoideae* and *Saccharomycoideae* (for example, genera *Pichia, Kluyveromyces* and *Saccharomyces*). The *Basidiosporogenous* yeasts include the genera *Leucosporidim, Rhodosporidium, Sporidiobolus, Filobasidium* and *Filobasidiella*. Yeast belonging to the *Fungi Imperfecti* are divided into two families, *Sporobolomycetaceae* (for example, genera *Sorobolomyces* and *Bullera*) and *Cryptococcaceae* (for example, genus *Candida*). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast (Skinner *et al.*, *Soc. App. Bacteriol. Symposium Series* No. 9, (1980), the entirety of which is herein incorporated by reference). The biology of yeast and manipulation of yeast genetics are well known in the art (*see,* for example, *Biochemistry and Genetics of Yeast,* Bacil *et al.* (ed.), 2nd edition, 1987; *The Yeasts*, Rose and Harrison (eds.), 2nd ed., (1987); and *The Molecular Biology of the Yeast Saccharomyces*, Strathern *et al.* (eds.), (1981), all of which are herein incorporated by reference in their entirety).

"Fungi" as used herein includes the phyla *Ascomycota, Basidiomycota, Chytridiomycota* and *Zygomycota* (as defined by Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK; the entirety of which is herein incorporated by reference) as well as the *Oomycota* (as cited in Hawksworth *et al.,* In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK) and all mitosporic fungi (Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK). Representative groups of *Ascomycota* include, for example, *Neurospora, Eupenicillium* (= *Penicillium*), *Emericella* (= *Aspergillus*), *Eurotiun* (= *Aspergillus*) and the true yeasts listed above. Examples of *Basidiomycota* include mushrooms, rusts and smuts. Representative groups of *Chytridiomycota* include, for example, *Allomyces, Blastocladiella, Coelomomyces* and aquatic fungi. Representative groups of *Oomycota* include, for example, *Saprolegniomycetous* aquatic fungi (water molds) such as *Achlya.* Examples of mitosporic fungi include *Aspergillus, Penicilliun, Candida* and *Alternaria.* Representative groups of *Zygomycota* include, for example, *Rhizopus* and *Mucor.*

"Filamentous fungi" include all filamentous forms of the subdivision *Eumycota* and *Oomycota* (as defined by Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK). The filamentous fungi are characterized by a vegetative mycelium composed of chitin, cellulose, glucan, chitosan, mannan and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

In one embodiment, the fungal host cell is a yeast cell. In a preferred embodiment, the yeast host cell is a cell of the species of *Candida, Kluyveromyces, Saccharomyces, Schizosaccharomyces, Pichia* and *Yarrowia.* In a preferred embodiment, the yeast host cell is a *Saccharomyces cerevisiae* cell, a *Saccharomyces carlsbergensis*, *Saccharomyces diastaticus* cell, a *Saccharomyces douglasii* cell, a *Saccharomyces kluyveri* cell, a *Saccharomyces norbensis* cell, or a *Saccharomyces oviformis* cell. In another preferred embodiment, the yeast host cell is a *Kluyveromyces lactis* cell. In another preferred embodiment, the yeast host cell is a *Yarrowia lipolytica* cell.

In another embodiment, the fungal host cell is a filamentous fungal cell. In a preferred embodiment, the filamentous fungal host cell is a cell of the species of, but not limited to, *Acremonium, Aspergillus, Fusarium, Humicola, Myceliophthora, Mucor, Neurospora, Penicillium, Thielavia, Tolypocladium* and *Trichoderma.* In a preferred embodiment, the filamentous fungal host cell is an *Aspergillus* cell. In another preferred embodiment, the filamentous fungal host cell is an *Acremonium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Fusarium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Humicola* cell. In another preferred embodiment, the filamentous fungal host cell is a *Myceliophthora* cell. In another even preferred embodiment, the filamentous fungal host cell is a *Mucor* cell. In another preferred embodiment, the filamentous fungal host cell is a *Neurospora* cell. In another preferred embodiment, the filamentous fungal host cell is a *Penicillium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Thielavia* cell. In another preferred embodiment, the filamentous fungal host cell is a *Tolypocladiun* cell. In another preferred embodiment, the filamentous fungal host cell is a *Trichoderma* cell. In a preferred embodiment, the filamentous fungal host cell is an *Aspergillus*

oryzae cell, an *Aspergillus niger* cell, an *Aspergillus foetidus* cell, or an *Aspergillus japonicus* cell. In another preferred embodiment, the filamentous fungal host cell is a *Fusarium oxysporum* cell or a *Fusarium graminearum* cell. In another preferred embodiment, the filamentous fungal host cell is a *Humicola insolens* cell or a *Humicola lanuginosus* cell. In another preferred embodiment, the filamentous fungal host cell is a *Myceliophthora thermophila* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Mucor miehei* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Neurospora crassa* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Penicillium purpurogenum* cell. In another most preferred embodiment, the filamentous fungal host cell is a *Thielavia terrestris* cell. In another most preferred embodiment, the *Trichoderma* cell is a *Trichoderma reesei* cell, a *Trichoderna viride* cell, a *Trichoderma longibrachiatum* cell, a *Trichoderma harzianum* cell, or a *Trichoderma koningii* cell. In a preferred embodiment, the fungal host cell is selected from an *A. nidulans* cell, an *A. niger* cell, an *A. oryzae* cell and an *A. sojae* cell. In a further preferred embodiment, the fungal host cell is an *A. nidulans* cell.

The recombinant fungal host cells of the present invention may further comprise one or more sequences which encode one or more factors that are advantageous in the expression of the protein or fragment thereof, for example, an activator (e.g., a trans-acting factor), a chaperone and a processing protease. The nucleic acids encoding one or more of these factors are preferably not operably linked to the nucleic acid encoding the protein or fragment thereof. An activator is a protein which activates transcription of a nucleic acid sequence encoding a polypeptide (Kudla *et al., EMBO* 9:1355-1364(1990); Jarai and Buxton, *Current Genetics* 26:2238-244(1994); Verdier, *Yeast 6*:271-297(1990), all of which are herein incorporated by reference in their entirety). The nucleic acid sequence encoding an activator may be obtained

from the genes encoding *Saccharomyces cerevisiae* heme activator protein 1 (hap1), *Saccharomyces cerevisiae* galactose metabolizing protein 4 (gal4) and *Aspergillus nidulans* ammonia regulation protein (areA). For further examples, see Verdier, *Yeast 6*:271-297 (1990); MacKenzie *et al., Journal of Gen. Microbiol. 139*:2295-2307 (1993), both of which are herein incorporated by reference in their entirety). A chaperone is a protein which assists another protein in folding properly (Hartl *et al., TIBS 19*:20-25 (1994); Bergeron *et al., TIBS* 19:124-128 (1994); Demolder *et al., J. Biotechnology* 32:179-189 (1994); Craig, *Science 260*:1902-1903(1993); Gething and Sambrook, *Nature* 355:33-45 (1992); Puig and Gilbert, *J Biol. Chem. 269*:7764-7771 (1994); Wang and Tsou, *FASEB Journal* 7:1515-11157 (1993); Robinson *et al., Bio/Technology 1*:381-384 (1994), all of which are herein incorporated by reference in their entirety). The nucleic acid sequence encoding a chaperone may be obtained from the genes encoding *Aspergillus oryzae* protein disulphide isomerase, *Saccharomyces cerevisiae* calnexin, *Saccharomyces cerevisiae* BiP/GRP78 and *Saccharomyces cerevisiae* Hsp70. For further examples, *see* Gething and Sambrook, *Nature 355*:33-45 (1992); Hartl *et al., TIBS 19*:20-25 (1994). A processing protease is a protease that cleaves a propeptide to generate a mature biochemically active polypeptide (Enderlin and Ogrydziak, *Yeast 10*:67-79 (1994); Fuller *et al., Proc. Natl. Acad. Sci. (U.S.A.) 86*:1434-1438 (1989); Julius *et al., Cell 37*:1075-1089 (1984); Julius *et al., Cell 32*:839-852 (1983), all of which are incorporated by reference in their entirety). The nucleic acid sequence encoding a processing protease may be obtained from the genes encoding *Aspergillus niger* Kex2, *Saccharomyces cerevisiae* dipeptidylaminopeptidase, *Saccharomyces cerevisiae* Kex2 and *Yarrowia lipolytica* dibasic processing endoprotease (xpr6). Any factor that is functional in the fungal host cell of choice may be used in the present invention.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts and regeneration of the cell wall in a manner known per se. Suitable procedures for transformation of *Aspergillus* host cells are described in EP 238 023 and Yelton *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 81*:1470-1474 (1984), both of which are herein incorporated by reference in their entirety. A suitable method of transforming *Fusarium* species is described by Malardier *et al.*, *Gene 78:*147-156 (1989), the entirety of which is herein incorporated by reference. Yeast may be transformed using the procedures described by Becker and Guarente, In: Abelson and Simon, (eds.), *Guide to Yeast Genetics and Molecular Biology, Methods Enzymol.* Volume 194, pp 182-187, Academic Press, Inc., New York; Ito *et al.*, *J. Bacteriology 153*:163 (1983); Hinnen *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 75*:1920 (1978), all of which are herein incorporated by reference in their entirety.

The present invention also relates to methods of producing the protein or fragment thereof comprising culturing the recombinant fungal host cells under conditions conducive for expression of the protein or fragment thereof. The fungal cells of the present invention are cultivated in a nutrient medium suitable for production of the protein or fragment thereof using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the protein or fragment thereof to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art (*see, e.g.*, Bennett and LaSure (eds.), *More Gene Manipulations in Fungi*, Academic Press, CA, (1991), the entirety of which is herein incorporated by reference). Suitable media are available from commercial suppliers or may be

prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection, Manassas, VA). If the protein or fragment thereof is secreted into the nutrient medium, a protein or fragment thereof can be recovered directly from the medium. If the protein or fragment thereof is not secreted, it is recovered from cell lysates.

The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein or fragment thereof are available, immunoassays may be employed using the antibodies to the protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known to those skilled in the art.

The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be further purified by a variety of chromatographic procedures, e.g., ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like.

(c) Mammalian Constructs and Transformed Mammalian Cells

The present invention also relates to methods for obtaining a recombinant mammalian host cell, comprising introducing into a mammalian host cell exogenous genetic material. The present invention also relates to a mammalian cell comprising a mammalian recombinant vector. The present invention also relates to methods for obtaining a recombinant mammalian host cell,

comprising introducing into a mammalian cell exogenous genetic material. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC, Manassas, VA), such as HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney (BHK) cells and a number of other cell lines. Suitable promoters for mammalian cells are also known in the art and include viral promoters such as that from Simian Virus 40 (SV40) (Fiers *et al.*, *Nature* 273:113 (1978), the entirety of which is herein incorporated by reference), Rous sarcoma virus (RSV), adenovirus (ADV) and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences and poly-A addition sequences. Enhancer sequences which increase expression may also be included and sequences which promote amplification of the gene may also be desirable (for example methotrexate resistance genes).

Vectors suitable for replication in mammalian cells may include viral replicons, or sequences which insure integration of the appropriate sequences encoding HCV epitopes into the host genome. For example, another vector used to express foreign DNA is vaccinia virus. In this case, for example, a nucleic acid molecule encoding a protein or fragment thereof is inserted into the vaccinia genome. Techniques for the insertion of foreign DNA into the vaccinia virus genome are known in the art and may utilize, for example, homologous recombination. Such heterologous DNA is generally inserted into a gene which is non-essential to the virus, for example, the thymidine kinase gene (tk), which also provides a selectable marker. Plasmid

vectors that greatly facilitate the construction of recombinant viruses have been described (*see*, for example, Mackett *et al*, *J Virol.* *49*:857 (1984); Chakrabarti *et al.*, *Mol. Cell. Biol.* *5*:3403 (1985); Moss, In: *Gene Transfer Vectors For Mammalian Cells* (Miller and Calos, eds., Cold Spring Harbor Laboratory, N.Y., p. 10, (1987); all of which are herein incorporated by reference in their entirety). Expression of the HCV polypeptide then occurs in cells or animals which are infected with the live recombinant vaccinia virus.

The sequence to be integrated into the mammalian sequence may be introduced into the primary host by any convenient means, which includes calcium precipitated DNA, spheroplast fusion, transformation, electroporation, biolistics, lipofection, microinjection, or other convenient means. Where an amplifiable gene is being employed, the amplifiable gene may serve as the selection marker for selecting hosts into which the amplifiable gene has been introduced. Alternatively, one may include with the amplifiable gene another marker, such as a drug resistance marker, e.g. neomycin resistance (G418 in mammalian cells), hygromycin in resistance etc., or an auxotrophy marker (HIS3, TRP1, LEU2, URA3, ADE2, LYS2, etc.) for use in yeast cells.

Depending upon the nature of the modification and associated targeting construct, various techniques may be employed for identifying targeted integration. Conveniently, the DNA may be digested with one or more restriction enzymes and the fragments probed with an appropriate DNA fragment which will identify the properly sized restriction fragment associated with integration.

One may use different promoter sequences, enhancer sequences, or other sequence which will allow for enhanced levels of expression in the expression host. Thus, one may combine an enhancer from one source, a promoter region from another source, a 5'- noncoding region

upstream from the initiation methionine from the same or different source as the other sequences and the like. One may provide for an intron in the non-coding region with appropriate splice sites or for an alternative 3'- untranslated sequence or polyadenylation site. Depending upon the particular purpose of the modification, any of these sequences may be introduced, as desired.

Where selection is intended, the sequence to be integrated will have with it a marker gene, which allows for selection. The marker gene may conveniently be downstream from the target gene and may include resistance to a cytotoxic agent, e.g. antibiotics, heavy metals, or the like, resistance or susceptibility to HAT, gancyclovir, etc., complementation to an auxotrophic host, particularly by using an auxotrophic yeast as the host for the subject manipulations, or the like. The marker gene may also be on a separate DNA molecule, particularly with primary mammalian cells. Alternatively, one may screen the various transformants, due to the high efficiency of recombination in yeast, by using hybridization analysis, PCR, sequencing, or the like.

For homologous recombination, constructs can be prepared where the amplifiable gene will be flanked, normally on both sides with DNA homologous with the DNA of the target region. Depending upon the nature of the integrating DNA and the purpose of the integration, the homologous DNA will generally be within 100kb, usually 50kb, preferably about 25kb, of the transcribed region of the target gene, more preferably within 2kb of the target gene. Where modeling of the gene is intended, homology will usually be present proximal to the site of the mutation. The homologous DNA may include the 5'-upstream region outside of the transcriptional regulatory region or comprising any enhancer sequences, transcriptional initiation sequences, adjacent sequences, or the like. The homologous region may include a portion of the coding region, where the coding region may be comprised only of an open reading frame or

combination of exons and introns. The homologous region may comprise all or a portion of an intron, where all or a portion of one or more exons may also be present. Alternatively, the homologous region may comprise the 3'-region, so as to comprise all or a portion of the transcriptional termination region, or the region 3' of this region. The homologous regions may extend over all or a portion of the target gene or be outside the target gene comprising all or a portion of the transcriptional regulatory regions and/or the structural gene.

The integrating constructs may be prepared in accordance with conventional ways, where sequences may be synthesized, isolated from natural sources, manipulated, cloned, ligated, subjected to in vitro mutagenesis, primer repair, or the like. At various stages, the joined sequences may be cloned and analyzed by restriction analysis, sequencing, or the like. Usually during the preparation of a construct where various fragments are joined, the fragments, intermediate constructs and constructs will be carried on a cloning vector comprising a replication system functional in a prokaryotic host, e.g., *E. coli* and a marker for selection, e.g., biocide resistance, complementation to an auxotrophic host, etc. Other functional sequences may also be present, such as polylinkers, for ease of introduction and excision of the construct or portions thereof, or the like. A large number of cloning vectors are available such as pBR322, the pUC series, etc. These constructs may then be used for integration into the primary mammalian host.

In the case of the primary mammalian host, a replicating vector may be used. Usually, such vector will have a viral replication system, such as SV40, bovine papilloma virus, adenovirus, or the like. The linear DNA sequence vector may also have a selectable marker for identifying transfected cells. Selectable markers include the neo gene, allowing for selection

with G418, the herpes tk gene for selection with HAT medium, the gpt gene with mycophenolic acid, complementation of an auxotrophic host, etc.

The vector may or may not be capable of stable maintenance in the host. Where the vector is capable of stable maintenance, the cells will be screened for homologous integration of the vector into the genome of the host, where various techniques for curing the cells may be employed. Where the vector is not capable of stable maintenance, for example, where a temperature sensitive replication system is employed, one may change the temperature from the permissive temperature to the non-permissive temperature, so that the cells may be cured of the vector. In this case, only those cells having integration of the construct comprising the amplifiable gene and, when present, the selectable marker, will be able to survive selection.

Where a selectable marker is present, one may select for the presence of the targeting construct by means of the selectable marker. Where the selectable marker is not present, one may select for the presence of the construct by the amplifiable gene. For the neo gene or the herpes tk gene, one could employ a medium for growth of the transformants of about 0.1-1 mg/ml of G418 or may use HAT medium, respectively. Where DHFR is the amplifiable gene, the selective medium may include from about 0.01-0.5 μM of methotrexate or be deficient in glycine-hypoxanthine-thymidine and have dialysed serum (GHT media).

The DNA can be introduced into the expression host by a variety of techniques that include calcium phosphate/DNA co-precipitates, microinjection of DNA into the nucleus, electroporation, yeast protoplast fusion with intact cells, transfection, polycations, e.g., polybrene, polyornithine, etc., or the like. The DNA may be single or double stranded DNA, linear or circular. The various techniques for transforming mammalian cells are well known (see Keown *et al.*, *Methods Enzymol.* (1989); Keown *et al.*, *Methods Enzymol.* *185*:527-537 (1990);

Mansour *et al., Nature 336*:348-352, (1988); all of which are herein incorporated by reference in their entirety).

(d) Insect Constructs and Transformed Insect Cells

The present invention also relates to an insect recombinant vectors comprising exogenous genetic material. The present invention also relates to an insect cell comprising an insect recombinant vector. The present invention also relates to methods for obtaining a recombinant insect host cell, comprising introducing into an insect cell exogenous genetic material. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention.

The insect recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleic acid sequence. The choice of a vector will typically depend on the compatibility of the vector with the insect host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the insect host. In addition, the insect vector may be an expression vector. Nucleic acid molecules can be suitably inserted into a replication vector for expression in the insect cell under a suitable promoter for insect cells. Many vectors are available for this purpose and selection of the appropriate vector will depend mainly on the size of the nucleic acid molecule to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and

the particular host cell with which it is compatible. The vector components for insect cell transformation generally include, but are not limited to, one or more of the following: a signal sequence, origin of replication, one or more marker genes and an inducible promoter.

The insect vector may be an autonomously replicating vector, *i.e.,* a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.,* a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the insect cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. For integration, the vector may rely on the nucleic acid sequence of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the insect host. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences which individually contain a sufficient number of nucleic acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. These nucleic acid sequences may be any sequence that is homologous with a target sequence in the genome of the insect host cell and, furthermore, may be non-encoding or encoding sequences.

Baculovirus expression vectors (BEVs) have become important tools for the expression of foreign genes, both for basic research and for the production of proteins with direct clinical

applications in human and veterinary medicine (Doerfler, *Curr. Top. Microbiol. Immunol. 131*:51-68 (1968); Luckow and Summers, *Bio/Technology 6*:47-55 (1988a); Miller, *Annual Review of Microbiol. 42*:177-199 (1988); Summers, *Curr. Comm. Molecular Biology*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1988); all of which are herein incorporated by reference in their entirety). BEVs are recombinant insect viruses in which the coding sequence for a chosen foreign gene has been inserted behind a baculovirus promoter in place of the viral gene, e.g., polyhedrin (Smith and Summers, U.S. Pat. No., 4,745,051, the entirety of which is incorporated herein by reference).

The use of baculovirus vectors relies upon the host cells being derived from *Lepidopteran* insects such as *Spodoptera frugiperda* or *Trichoplusia ni*. The preferred *Spodoptera frugiperda* cell line is the cell line Sf9. The *Spodoptera frugiperda* Sf9 cell line was obtained from American Type Culture Collection (Manassas, VA.) and is assigned accession number ATCC CRL 1711 (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), the entirety of which is herein incorporated by reference). Other insect cell systems, such as the silkworm *B. mori* may also be used.

The proteins expressed by the BEVs are, therefore, synthesized, modified and transported in host cells derived from *Lepidopteran* insects. Most of the genes that have been inserted and produced in the baculovirus expression vector system have been derived from vertebrate species. Other baculovirus genes in addition to the polyhedrin promoter may be employed to advantage in a baculovirus expression system. These include immediate-early (alpha), delayed-early (β), late (γ), or very late (delta), according to the phase of the viral infection during which they are expressed. The expression of these genes occurs sequentially, probably as the result of a

"cascade" mechanism of transcriptional regulation. (Guarino and Summers, *J. Virol. 57*:563-571 (1986); Guarino and Summers, *J. Virol. 61*:2091-2099 (1987); Guarino and Summers, *Virol. 162*:444-451 (1988); all of which are herein incorporated by reference in their entirety).

Insect recombinant vectors are useful as intermediates for the infection or transformation of insect cell systems. For example, an insect recombinant vector containing a nucleic acid molecule encoding a baculovirus transcriptional promoter followed downstream by an insect signal DNA sequence is capable of directing the secretion of the desired biologically active protein from the insect cell. The vector may utilize a baculovirus transcriptional promoter region derived from any of the over 500 baculoviruses generally infecting insects, such as for example the Orders *Lepidoptera, Diptera, Orthoptera, Coleoptera and Hymenoptera*, including for example but not limited to the viral DNAs of *Autographa californica MNPV, Bombyx mori NPV, Trichoplusia ni MNPV, Rachiplusia ou MNPV or Galleria mellonella MNPV*, wherein said baculovirus transcriptional promoter is a baculovirus immediate-early gene IEl or IEN promoter; an immediate-early gene in combination with a baculovirus delayed-early gene promoter region selected from the group consisting of 39K and a *HindIII-k* fragment delayed-early gene; or a baculovirus late gene promoter. The immediate-early or delayed-early promoters can be enhanced with transcriptional enhancer elements. The insect signal DNA sequence may code for a signal peptide of a *Lepidopteran* adipokinetic hormone precursor or a signal peptide of the *Manduca sexta* adipokinetic hormone precursor (Summers, U.S. Patent No. 5,155,037; the entirety of which is herein incorporated by reference). Other insect signal DNA sequences include a signal peptide of the *Orthoptera Schistocerca gregaria* locust adipokinetic hormone precurser and the *Drosophila melanogaster* cuticle genes CP1, CP2, CP3 or CP4 or for an insect

signal peptide having substantially a similar chemical composition and function (Summers, U.S. Patent No. 5,155,037).

Insect cells are distinctly different from animal cells. Insects have a unique life cycle and have distinct cellular properties such as the lack of intracellular plasminogen activators in which are present in vertebrate cells. Another difference is the high expression levels of protein products ranging from 1 to greater than 500 mg/liter and the ease at which cDNA can be cloned into cells (Frasier, *In Vitro Cell. Dev. Biol. 25*:225 (1989); Summers and Smith, In: *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), both of which are incorporated by reference in their entirety).

Recombinant protein expression in insect cells is achieved by viral infection or stable transformation. For viral infection, the desired gene is cloned into baculovirus at the site of the wild-type polyhedron gene (Webb and Summers, *Technique 2*:173 (1990); Bishop and Posse, *Adv. Gene Technol. 1*:55 (1990); both of which are incorporated by reference in their entirety). The polyhedron gene is a component of a protein coat in occlusions which encapsulate virus particles. Deletion or insertion in the polyhedron gene results the failure to form occlusion bodies. Occlusion negative viruses are morphologically different from occlusion positive viruses and enable one skilled in the art to identify and purify recombinant viruses.

The vectors of present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs and the like. Selection may be accomplished by co-transformation, *e.g.*, as described in WO 91/17243, a nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence which is

recognized by the insect host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the protein or fragment thereof. The promoter may be any nucleic acid sequence which shows transcriptional activity in the insect host cell of choice and may be obtained from genes encoding polypeptides either homologous or heterologous to the host cell.

For example, a nucleic acid molecule encoding a protein or fragment thereof may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the insect host cell of choice may be used in the present invention.

A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the insect host to add polyadenosine residues to transcribed mRNA. The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the fungal host of choice may be used in the present invention.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and to minimize the amount of possible degradation of the expressed polypeptide within the cell, it is preferred that expression of the polypeptide gene gives rise to a product secreted outside the cell. To this end, the protein or fragment thereof of the present invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an

amino acid sequence which permits the secretion of the protein or fragment thereof from the insect host into the culture medium. The signal peptide may be native to the protein or fragment thereof of the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the present invention may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof.

At present, a mode of achieving secretion of a foreign gene product in insect cells is by way of the foreign gene's native signal peptide. Because the foreign genes are usually from non-insect organisms, their signal sequences may be poorly recognized by insect cells and hence, levels of expression may be suboptimal. However, the efficiency of expression of foreign gene products seems to depend primarily on the characteristics of the foreign protein. On average, nuclear localized or non-structural proteins are most highly expressed, secreted proteins are intermediate and integral membrane proteins are the least expressed. One factor generally affecting the efficiency of the production of foreign gene products in a heterologous host system is the presence of native signal sequences (also termed presequences, targeting signals, or leader sequences) associated with the foreign gene. The signal sequence is generally coded by a DNA sequence immediately following (5' to 3') the translation start site of the desired foreign gene.

The expression dependence on the type of signal sequence associated with a gene product can be represented by the following example: If a foreign gene is inserted at a site downstream from the translational start site of the baculovirus polyhedrin gene so as to produce a fusion protein (containing the N-terminus of the polyhedrin structural gene), the fused gene is highly expressed. But less expression is achieved when a foreign gene is inserted in a baculovirus

expression vector immediately following the transcriptional start site and totally replacing the polyhedrin structural gene.

Insertions into the region -50 to -1 significantly alter (reduce) steady state transcription which, in turn, reduces translation of the foreign gene product. Use of the pVL941 vector optimizes transcription of foreign genes to the level of the polyhedrin gene transcription. Even though the transcription of a foreign gene may be optimal, optimal translation may vary because of several factors involving processing: signal peptide recognition, mRNA and ribosome binding, glycosylation, disulfide bond formation, sugar processing, oligomerization, for example.

The properties of the insect signal peptide are expected to be more optimal for the efficiency of the translation process in insect cells than those from vertebrate proteins. This phenomenon can generally be explained by the fact that proteins secreted from cells are synthesized as precursor molecules containing hydrophobic N-terminal signal peptides. The signal peptides direct transport of the select protein to its target membrane and are then cleaved by a peptidase on the membrane, such as the endoplasmic reticulum, when the protein passes through it.

Another exemplary insect signal sequence is the sequence encoding for Drosophila cuticle proteins such as CP1, CP2, CP3 or CP4 (Summers, U.S. Patent No. 5,278,050; the entirety of which is herein incorporated by reference). Most of a 9kb region of the Drosophila genome containing genes for the cuticle proteins has been sequenced. Four of the five cuticle genes contains a signal peptide coding sequence interrupted by a short intervening sequence (about 60 base pairs) at a conserved site. Conserved sequences occur in the 5' mRNA untranslated region, in the adjacent 35 base pairs of upstream flanking sequence and at -200 base pairs from the mRNA start position in each of the cuticle genes.

Standard methods of insect cell culture, cotransfection and preparation of plasmids are set forth in Summers and Smith (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures*, Texas Agricultural Experiment Station Bulletin No. 1555, Texas A&M University (1987)). Procedures for the cultivation of viruses and cells are described in Volkman and Summers, *J. Virol 19*:820-832 (1975) and Volkman *et al.*, *J. Virol 19*:820-832 (1976); both of which are herein incorporated by reference in their entirety.

(e) Bacterial Constructs and Transformed Bacterial Cells

The present invention also relates to a bacterial recombinant vector comprising exogenous genetic material. The present invention also relates to a bacteria cell comprising a bacterial recombinant vector. The present invention also relates to methods for obtaining a recombinant bacteria host cell, comprising introducing into a bacterial host cell exogenous genetic material.. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention.

The bacterial recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the bacterial host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the bacterial host. In addition, the bacterial vector may be an expression vector. Nucleic acid molecules encoding protein homologues or fragments thereof can, for example, be suitably inserted into a replicable vector for expression in the bacterium

under the control of a suitable promoter for bacteria. Many vectors are available for this purpose and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and the particular host cell with which it is compatible. The vector components for bacterial transformation generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes and an inducible promoter.

In general, plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell are used in connection with bacterial hosts. The vector ordinarily carries a replication site, as well as marking sequences that are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g., Bolivar *et al.*, *Gene* 2:95 (1977); the entirety of which is herein incorporated by reference). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid or phage, also generally contains, or is modified to contain, promoters that can be used by the microbial organism for expression of the selectable marker genes.

Nucleic acid molecules encoding protein or fragments thereof may be expressed not only directly, but also as a fusion with another polypeptide, preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the polypeptide DNA that is inserted into the vector. The heterologous signal sequence selected

should be one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. For bacterial host cells that do not recognize and process the native polypeptide signal sequence, the signal sequence is substituted by a bacterial signal sequence selected, for example, from the group consisting of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria.

Expression and cloning vectors also generally contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*. One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous protein homologue or fragment thereof produce a protein conferring drug resistance and thus survive the selection regimen.

The expression vector for producing a protein or fragment thereof can also contains an inducible promoter that is recognized by the host bacterial organism and is operably linked to the

nucleic acid encoding, for example, the nucleic acid molecule encoding the protein homologue or fragment thereof of interest. Inducible promoters suitable for use with bacterial hosts include the β-lactamase and lactose promoter systems (Chang *et al.*, *Nature 275*:615 (1978); Goeddel *et al.*, *Nature 281*:544 (1979); both of which are herein incorporated by reference in their entirety), the arabinose promoter system (Guzman *et al., J. Bacteriol. 174*:7716-7728 (1992); the entirety of which is herein incorporated by reference), alkaline phosphatase, a tryptophan (trp) promoter system (Goeddel, *Nucleic Acids Res. 8*:4057 (1980); EP 36,776; both of which are herein incorporated by reference in their entirety) and hybrid promoters such as the tac promoter (deBoer *et al.*, *Proc. Natl. Acad. Sci. (USA) 80*:21-25 (1983); the entirety of which is herein incorporated by reference). However, other known bacterial inducible promoters are suitable (Siebenlist *et al.*, *Cell 20*:269 (1980); the entirety of which is herein incorporated by reference).

Promoters for use in bacterial systems also generally contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the polypeptide of interest. The promoter can be removed from the bacterial source DNA by restriction enzyme digestion and inserted into the vector containing the desired DNA.

Construction of suitable vectors containing one or more of the above-listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored and re-ligated in the form desired to generate the plasmids required. Examples of available bacterial expression vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as Bluescript™ (Stratagene, La Jolla, CA), in which, for example, encoding an *A. nidulans* protein homologue or fragment thereof homologue, may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of

β-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke and Schuster, *J. Biol. Chem. 264*:5503-5509 (1989), the entirety of which is herein incorporated by reference); and the like. pGEX vectors (Promega, Madison Wisconsin U.S.A.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to include heparin, thrombin or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

Suitable host bacteria for a bacterial vector include archaebacteria and eubacteria, especially eubacteria and most preferably *Enterobacteriaceae*. Examples of useful bacteria include *Escherichia, Enterobacter, Azotobacter, Erwinia, Bacillus, Pseudomonas, Klebsiella, Proteus, Salmonella, Serratia, Shigella, Rhizobia, Vitreoscilla and Paracoccus*. Suitable *E. coli* hosts include *E. coli* W3110 (American Type Culture Collection (ATCC) 27,325, Manassas, Virginia U.S.A.), *E. coli* 294 (ATCC 31,446), *E. coli B* and *E. coli* X1776 (ATCC 31,537). These examples are illustrative rather than limiting. Mutant cells of any of the above-mentioned bacteria may also be employed. It is, of course, necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, *E. coli, Serratia*, or *Salmonella* species can be suitably used as the host when well known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon. *E. coli* strain W3110 is a preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell should secrete minimal amounts of proteolytic enzymes.

Host cells are transfected and preferably transformed with the above-described vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

Numerous methods of transfection are known to the ordinarily skilled artisan, for example, calcium phosphate and electroporation. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, (1989), is generally used for bacterial cells that contain substantial cell-wall barriers. Another method for transformation employs polyethylene glycol/DMSO, as described in Chung and Miller (Chung and Miller, *Nucleic Acids Res. 16*:3580 (1988); the entirety of which is herein incorporated by reference). Yet another method is the use of the technique termed electroporation.

Bacterial cells used to produce the polypeptide of interest for purposes of this invention are cultured in suitable media in which the promoters for the nucleic acid encoding the heterologous polypeptide can be artificially induced as described generally, e.g., in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, (1989). Examples of suitable media are given in U.S. Pat. Nos. 5,304,472 and 5,342,763; both of which are incorporated by reference in their entirety.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook

et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995), the entirety of which is herein incorporated by reference; Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

(f) Computer Readable Media

The nucleotide sequence provided in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof, or complement thereof, or a nucleotide sequence at least 90% identical, preferably 95%, identical even more preferably 99% or 100% identical to the sequence provided in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof, or complement thereof, can be "provided" in a variety of mediums to facilitate use. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

A preferred subset of nucleotide sequences are those nucleic acid sequences that encode a first nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean

transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either.

A further preferred subset of nucleic acid sequences is where the subset of sequences which encode two proteins or fragments thereof, more preferably three proteins or fragments thereof, more preferable four proteins or fragments thereof, more preferably five proteins or fragments thereof, more preferably six proteins or fragments thereof, more preferably seven proteins or fragments thereof, more preferably eight proteins or fragments thereof, more preferably nine proteins or fragments thereof, more preferably ten proteins or fragments thereof, and even more preferably eleven proteins or fragments thereof. These nucleic acid sequences are selected from the group that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase

enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium and magnetic tape: optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will

generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990), the entirety of which is herein incorporated by reference) and BLAZE (Brutlag *et al., Comp. Chem. 17:*203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification and DNA replication, restriction, modification, recombination and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or

implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, “a target structural motif,” or “target motif,” refers to any rationally selected sequence or combination of sequences in which the sequences the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various

amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the present invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the present invention. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration and are not intended to be limiting of the present invention, unless specified.

Example 1

The MONN01 cDNA library is a normalized library generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and

the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when maize plants are at the 6-leaf development stage. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON001 cDNA library is generated from maize (B73, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) immature tassels at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tassel tissue from maize plants is collected at the V6 stage. At that stage the tassel is an immature tassel of about 2-3 cm in length. Tassels are removed and frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON003 library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) roots at the V6 developmental stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth, the seedlings are transplanted into 10 inch pots containing the Metro 200 growing medium. Plants are watered daily before transplantation and approximately 3 times a week after transplantation. Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting at a concentration of 150 ppm N. Two to three times during the life time of the plant from transplanting to flowering a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a green house in approximately 15hr day/9hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6 leaf development stage. The root system is cut from maize plant and washed with water to free it from the soil. The tissue is then immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON004 cDNA library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant,

from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON005 cDNA library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) root tissue at the V6 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The root system is cut from the mature maize plant and washed with water to free it from the

soil. The tissue is immediately frozen in liquid nitrogen and the harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON006 cDNA library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON007 cDNA library is generated from the primary root tissue of 5 day old maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a

moist filter paper on a covered tray that is kept in the dark until germination (one day). After germination, the trays, along with the moist paper, are moved to a greenhouse where the maize plants are grown in the greenhouse in 15 hr day/9 hr night cycles for approximately 5 days. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. The primary root tissue is collected when the seedlings are 5 days old. At this stage, the primary root (radicle) is pushed through the coleorhiza which itself is pushed through the seed coat. The primary root, which is about 2-3 cm long, is cut and immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON008 cDNA library is generated from the primary shoot (coleoptile 2-3 cm) of maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings which are approximately 5 days old. Seeds are planted on a moist filter paper on a covered tray that is kept in the dark until germination (one day). Then the trays containing the seeds are moved to a greenhouse at 15hr daytime/9 hr nighttime cycles and grown until they are 5 days post germination. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Tissue is collected when the seedlings are 5 days old. At this stage, the primary shoot (coleoptile) is pushed through the seed coat and is about 2-3 cm long. The coleoptile is dissected away from the rest of the seedling, immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON009 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaves at the 8 leaf stage (V8 plant development stage). Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 8-leaf development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical, are cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON010 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) root tissue at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a

strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the V8 development stage. The root system is cut from this mature maize plant and washed with water to free it from the soil. The tissue is immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON011 cDNA library is generated from undeveloped maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaf at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The second youngest leaf which is at the base of the apical leaf of V6 stage maize plant is cut at the base and immediately transferred to liquid nitrogen containers in which the leaf is crushed. The harvested

tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON012 cDNA library is generated from 2 day post germination maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a moist filter paper on a covered tray that is kept in the dark until germination (one day). Then the trays containing the seeds are moved to the greenhouse and grown at 15hr daytime/9 hr nighttime cycles until 2 days post germination. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Tissue is collected when the seedlings are 2 days old. At the two day stage, the coleorhiza is pushed through the seed coat and the primary root (the radicle) is pierced the coleorhiza but is barely visible. Also, at this two day stage, the coleoptile is just emerging from the seed coat. The 2 days post germination seedlings are then immersed in liquid nitrogen and crushed. The harvested tissue is stored at –80°C until preparation of total RNA. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON013 cDNA library is generated from apical maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) meristem founder at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a

greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Prior to tissue collection, the plant is at the 4 leaf stage. The lead at the apex of the V4 stage maize plant is referred to as the meristem founder. This apical meristem founder is cut, immediately frozen in liquid nitrogen and crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON014 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) endosperm at fourteen days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, ear shoots are ready for fertilization. At this stage, the ear shoots are enclosed in a paper bag before silk emergence to withhold the pollen. The ear shoots are pollinated and 14 days after pollination, the ears are pulled out and then the kernels are plucked out of the ears. Each kernel is then dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the endosperms are immediately frozen in liquid

nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON016 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) sheath tissue collected at the V8 developmental stage. Seeds are planted in a depth of approximately 3 cm in solid into 2-3 inch pots containing Metro growing medium. After 2-3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and approximately the times a week after transplantation. Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting, at a strength of 150 ppm N. Two to three times during the life time of the plant from transplanting to flowering, a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15hr day/9hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. When the maize plants are at the V8 stage the 5th and 6th leaves from the bottom exhibit fully developed leaf blades. At the base of these leaves, the ligule is differentiated and the leaf blade is joined to the sheath. The sheath is dissected away from the base of the leaf then the sheath is frozen in liquid nitrogen and crushed. The tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON017 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) embryo collected from plants at twenty one days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth the seeds are transplanted into 10 inch pots containing

the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of maize plant, which are ready for fertilization, are enclosed in a paper bag before silk emergence to withhold the pollen. The ear shoots are fertilized and 21 days after pollination, the ears are pulled out and the kernels are plucked out of the ears. Each kernel is then dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the embryos are immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON019 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) culm (stem) at the V8 developmental stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is

approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. When the maize plant is at the V8 stage, the 5th and 6th leaves from the bottom have fully developed leaf blades. The region between the nodes of the 5th and the sixth leaves from the bottom is the region of the stem that is collected. The leaves are pulled out and the sheath is also torn away from the stem. This stem tissue is completely free of any leaf and sheath tissue. The stem tissue is then frozen in liquid nitrogen and stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON020 cDNA library is from a maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) Hill Type II-Initiated Callus. Petri plates containing approximately 25 ml of Type II initiation media are prepared. This medium contains N6 salts and vitamins, 3% sucrose, 2.3 g/liter proline 0.1 g/liter enzymatic casein hydrolysate, 2mg/liter 2,4 – dichloro phenoxy-acetic acid (2,4, D), 15.3 mg/liter $AgNO_3$ and 0.8% bacto agar and is adjusted to pH 6.0 before autoclaving. At 9-11 days after pollination, an ear with immature embryos measuring approximately 1-2 mm in length is chosen. The husks and silks are removed and then the ear is broken into halves and placed in an autoclaved solution of Clorox/TWEEN 20 sterilizing solution. Then the ear is rinsed with deionized water. Then each embryo is extracted from the kernel. Intact embryos are placed in contact with the medium, scutellar side up). Multiple embryos are plated on each plate and the plates are incubated in the dark at 25°C. Type II calluses are friable, can be subcultured with a spatula, frequently regenerate via somatic embryogenesis and are relatively undifferentiated. As seen in the microscope, the Tape II calluses show color ranging from translucent to light yellow and heterogeneity on with respect to embryoid structure as well as stage of embryoid development. Once Type II callus are formed,

the calluses is transferred to type II callus maintenance medium without $AgNO_3$. Every 7-10 days, the callus is subcultured. About 4 weeks after embryo isolation the callus is removed from the plates and then frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON021 cDNA library is generated from the immature maize (DK604, Dekalb Genetics, Dekalb Illinois, U.S.A.) tassel at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. As the maize plant enters the V8 stage, tassels which are 15-20 cm in length are collected and frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON022 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) immature ear at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the plant is in the V8 stage. At this stage, some immature ear shoots are visible. The immature ear shoots (approximately 3-4 cm in length) are pulled out, frozen in liquid nitrogen and then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON023 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) ear (growing silk) at the V8 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. When the tissue is harvested at the V8 stage, the length of the ear that is harvested is about 10-15 cm and the silks are just exposed (approximately 1 inch).

The ear along with the silks is frozen in liquid nitrogen and then the tissue is stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON024 cDNA library is generated from the immature maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) tassel at the V9 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. As a maize plant enters the V9 stage, the tassel is rapidly developing and a 37 cm tassel along with the glume, anthers and pollen is collected and frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON025 cDNA library is from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) Hill Type II-Regenerated Callus. Type II callus is grown in initiation media as described for SATMON020 and then the embryoids on the surface of the Type II callus are allowed to mature and germinate. The 1-2 gm fresh weight of the soft friable type callus containing numerous embryoids are transferred to 100 x 15 mm petri plates containing 25 ml of regeneration media. Regeneration media consists of Murashige and Skoog (MS) basal salts,

modified White's vitamins (0.2 g/liter glycine and 0.5 g/liter myo-inositoland 0.8% bacto agar (6SMS0D)). The plates are then placed in the dark after covering with parafilm. After 1 week, the plates are moved to a lighted growth chamber with 16 hr light and 8 hr dark photoperiod. Three weeks after plating the Type II callus to 6SMS0D, the callus exhibit shoot formation. The callus and the shoots are transferred to fresh 6SMS0D plates for another 2 weeks. The callus and the shoots are then transferred to petri plates with reduced sucrose (3SMSOD). Upon distinct formation of a root and shoot, the newly developed green plants are then removed out with a spatula and frozen in liquid nitrogen containers. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON026 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) juvenile/adult shift leaves at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plants are at the 8-leaf development stage. Leaves are founded sequentially around the meristem over weeks of time and the older, more juvenile leaves

arise earlier and in a more basal position than the younger, more adult leaves, which are in a more apical position. In a V8 plant, some leaves which are in the middle portion of the plant exhibit characteristics of both juvenile as well as adult leaves. They exhibit a yellowing color but also exhibit, in part, a green color. These leaves are termed juvenile/adult shift leaves. The juvenile/adult shift leaves (the 4th, 5th leaves from the bottom) are cut at the base, pooled and transferred to liquid nitrogen in which they are then crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON027 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaves from plants at the V8 developmental stage that are subject to six days water stress. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the Metro 200 growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Prior to tissue collection, when the plant is at the 8-leaf stage, water is held back for six days. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical, are all cut at the base of the leaves. All the leaves exhibit significant wilting. The leaves

are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON028 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) roots at the V8 developmental stage that are subject to six days water stress. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the Metro 200 growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Prior to tissue collection, when the plant is at the 8-leaf stage, water is held back for six days. The root system is cut, shaken and washed to remove soil. Root tissue is then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON029 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings at the etiolated stage. Seeds are planted on a moist filter paper

on a covered tray that is kept in the dark for 4 days at approximately 70°F. Tissue is collected when the seedlings are 4 days old. By 4 days, the primary root has penetrated the coleorhiza and is about 4-5 cm and the secondary lateral roots have also made their appearance. The coleoptile has also pushed through the seed coat and is about 4-5 cm long. The seedlings are frozen in liquid nitrogen and crushed. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON030 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) root tissue at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth, they are transplanted into 10 inch pots containing the same. Plants are watered daily before transplantation and approximately 3 times a week after transplantation. Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting, at a strength of 150 ppm N. Two to three times during the life time of the plant, from transplanting to flowering, a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15hr day/9hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 sodium vapor lamps. Tissue is collected when the maize plant is at the 4 leaf development stage. The root system is cut from the mature maize plant and washed with water to free it from the soil. The tissue is then immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON031 cDNA library is generated from the maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaf tissue at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 4-leaf development stage. The third leaf from the bottom is cut at the base and immediately frozen in liquid nitrogen and crushed. The tissue is immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON033 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) embryo tissue from plants at 13 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to

flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of the maize plant, which are ready for fertilization, are enclosed in a paper bag before silk emergent to withhold the pollen. The ear shoots are pollinated and 13 days after pollination, the ears are pulled out and then the kernels are plucked cut of the ears. Each kernel is then dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the embryos are immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON034 cDNA library is generated from cold stressed maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a moist filter paper on a covered tray that is kept on at 10°C for 7 days. After 7 days, the temperature is shifted to 15°C for one day until germination of the seed. Tissue is collected once the seedlings are 1 day old. At this point, the coleorhiza has just pushed out of the seed coat and the primary root is just making its appearance. The coleoptile has not yet pushed completely through the seed coat and is also just making its appearance. These 1 day old cold stressed seedlings are frozen in liquid nitrogen and crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMONN01 cDNA library is a normalized library generated from maize (B73, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) immature tassels at the V6 plant

development stage normalized tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue from the maize plant is collected at the V6 stage. At that stage the tassel is an immature tassel of about 2-3 cm in length. The tassels are removed and frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The SATMONN04 cDNA library is a normalized library generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is

approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The SATMONN05 cDNA library is a normalized library generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) root tissue at the V6 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The root system is cut from the mature maize plant and washed with water to free it from the soil. The tissue is immediately frozen in liquid nitrogen and the harvested

tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The SATMONN06 cDNA library is a normalized library generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

LIB36 is a normalized cDNA library prepared from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-

3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15hr day /9hr night cycles. The daytime temperature is 80°F and the night time temperature is 70°F. Lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V8 stage plants. The older more juvenile leaves which are in a basal position as well as the younger more adult leaves which are more apical were all cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at -80°C until RNA preparation.

For the construction of a cDNA library, the Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is purified from the total RNA preparation using Dynabeads® Oligo $(dT)_{25}$ (Dynal Inc., Lake Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using a commercially available kit for normalizing the cDNA library.

LIB83 is a normalized cDNA library prepared from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Plants are grown in a greenhouse in 15hr day /9hr night cycles. The daytime temperature is 80°F and the night time temperature was 70°F. Lighting was provided by 1000 W sodium vapor lamps. Tissue is collected from V8 stage plants. The older more juvenile leaves which are in a basal position as well as the younger more adult leaves which are more apical were all cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed The harvested tissue is then stored at -80°C until RNA preparation.

For the construction of a cDNA library, the Superscript ™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is purified from the total RNA preparation using Dynabeads® Oligo $(dT)_{25}$ (Dynal Inc., Lake Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using a commercially available kit for normalizing the cDNA library.

LIB84 a normalized cDNA library is prepared from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe

is added to each pot. Plants were grown in a greenhouse in 15hr day /9hr night cycles. The daytime temperature was 80°F and the night time temperature was70 °F. Lighting was provided by 1000 W sodium vapor lamps. Tissue was collected from V8 stage plants. The older more juvenile leaves which are in a basal position as well as the younger more adult leaves which are more apical were all cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at -80°C until RNA preparation.

For the construction of a cDNA library, the Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is purified from the total RNA preparation using Dynabeads® Oligo $(dT)_{25}$ (Dynal Inc., Lake Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using a commercially available kit for normalizing the cDNA library.

The CMz029 (SATMON036) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) endosperm 22 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime

temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of the maize plant, which are ready for fertilization, are enclosed in a paper bag before silk emergent to withhold the pollen. The ear shoots are pollinated and 22 days after pollination, the ears are pulled out and then the kernels are plucked out of the ears. Each kernel is then dissected into the embryo and the endosperm and the alurone layer is removed. After dissection, the endosperms are immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz030 (Lib143) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedling tissue two days post germination. Seeds are planted on a moist filter paper on a covered try that is keep in the dark until germination. The trays are then moved to the bench top at 15 hr daytime/9 hr nighttime cycles for 2 days post-germination. The day time temperature is 80°F and the nighttime temperature is 70°F. Tissue is collected when the seedlings are 2 days old. At this stage, the colehrhiza has pushed through the seed coat and the primary root (the radicle) is just piercing the colehrhiza and is barely visible. The seedlings are placed at 42°C for 1 hour. Following the heat shock treatment, the seedlings are immersed in liquid nitrogen and crushed. The harvested tissue is stored at –80° until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz031 (Lib148) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) pollen tissue at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag to withhold pollen. Twenty-one days after pollination, prior to removing the ears, the paper bag is shaken to collect the mature pollen. The mature pollen is immediately frozen in liquid nitrogen containers and the pollen is crushed. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz033 (Lib189) cDNA library is generated from maize (RX601 Asgrow, Asgrow Seed Company, Des Moines, Iowa U.S.A.) pooled leaf tissue harvested from field grown plants at Asgrow research stations. Leaves are harvested at anthesis from open pollinated plants in a field (mulitple row) setting. The ear leaves from 10-12 plants are harvested, pooled, frozen in liquid nitrogen and then frozen at -80C where they are stored until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz034 (Lib3060) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) senescing leaves from plants at 40 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200

growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from leaves located two leaves below the ear leaf. This sample represents those genes expressed during onset and early stages of leaf senescence. The leaves are pooled and immediately transferred to liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz035 (Lib3061) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) endosperm tissue from plants at 32 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°Fand the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag prior to silk emergence to withhold pollen. Thirty-two days after pollination, the ears are pulled out and the kernels are removed from the cob. Each kernel is dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the endosperms are immediately transferred to liquid nitrogen. The harvested tissue is then stored at 80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz036 (Lib3062) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urban, Illinois U.S.A.) husk tissue from 8 week old plants. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from 8 week old plants. The husk is separated from the ear and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz037 (Lib3059) cDNA library is generated from maize (RX601 Asgrow, Asgrow Seed Company, Des Moines, Iowa U.S.A) pooled kernels from plants at 12-15 days after pollination. Sample are collected from field grown material. Whole kernels from hand pollinated (control pollination) are harvested as whole ears and immediately frozen on dry ice. Kernels from 10-12 ears are pooled and ground together in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz039 (Lib3066) cDNA library is generated from maize (H99 USDA Maize Germplasm Collection, Urban, Illinois U.S.A.) immature anther tissue at the 7 week old immature tassel stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 7 week old immature tassel stage. At this stage, prior to anthesis, the immature anthers are green and enclosed in the staminate spikelet. The developing anthers are dissected away from the 7 week old immature tassel and immediately frozen in liquid nitrogen. The harvested tissue

is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz040 (Lib3067) cDNA library is generated from maize (MO17 USDA Maixe Germplasm Collection, Urbana, Illinois U.S.A.) kernel tissue from plants at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag before silk emergence to withhold pollen. Five to eight days after controlled pollination. The ears are pulled and the kernels removed. The kernels are immediately frozen in liquid nitrogen. This sample represents genes expressed in early kernel development, during periods of cell division, amyloplast biogenesis and early carbon flow across the material to filial tissue. The harvested kernels tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz041 (Lib3068) cDNA library is generated from maize pollen germinating silk tissue from plants at the V10+ plant development stage. Maize MO17 and H99 (USDA Maize

Germplasm Collection, Urbana, Illinois U.S.A.) seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants when the ear shoots are ready for fertilization at the silk emergence stage. The H99 emerging silks are pollinated with an excess of MO17 pollen under controlled pollination conditions in the green house. Eighteen hours after pollination the silks are removed from the ears and immediately frozen in liquid nitrogen. This sample represents genes expressed in both pollen and silk tissue early in pollination. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz042 (Lib3069) cDNA library is generated from maize ear tissue excessively pollinated at the V10+ plant development stage. Maize MO17 and H99 (USDA Maize Germplasm Collection, Urbana, Illinois U.S.A.) seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants and the ear shoots which are ready for fertilization are at the silk emergence stage. The H99 immature ears are pollinated with an excess of MO17 pollen under controlled pollination conditions. Eighteen hours post-pollination, the ears are removed and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz044 (Lib3075) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urbana, Illinois U.S.A.) microspore tissue from plants at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from immature anthers

from 7 week old tassels. The immature anthers are first dissected from the 7 week old tassel with a scalpel on a glass slide covered with water. The microspores (immature pollen) are released into the water and are recovered by centrifugation. The microspore suspension is immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz045 (Lib3076) cDNA library is generated from maize (H99 USDA Maize Germplasm Collection, Urbana, Illinois U.S.A.) immature ear megaspore tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. The immature ears are harvested from the 7 week old plants and are approximately 2.5 to 3 cm in length. The kernels are removed from the cob immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz047 (Lib3078) cDNA library is generated from maize (RX601, Asgrow Seed Company, Des Moines, Iowa, U.S.A.) CO_2 treated high-exposure shoot tissue at the V10+ plant

development stage. RX601 maize seeds are sterilized for 1 minute with a 10% Clorox solution. The seeds are rolled in germination paper, and germinated in 0.5 mM calcium sulfate solution for two days at 30°C. The seedlings are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium at a rate of 2-3 seedlings per pot. Twenty pots are placed into a high CO_2 environment (approximately 1000 ppm CO_2). Twenty plants were grown under ambient greenhouse CO_2 (approximately 450 ppm CO_2). Plants are hand watered. Peters 20-20-20 fertilizer is also lightly applied. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. At ten days post planting, the shoots from both atmosphere are frozen in liquid nitrogen and lightly ground. The roots are washed in deionized water to remove the support media and the tissue is immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz048 (Lib3079) cDNA library is generated from maize (MO17USDA Maize Germplasm Collection, Urbana, Illinois U.S.A) basal endosperm transfer layer tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in

15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ maize plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag prior to silk emergence, to withhold the pollen. Kernels are harvested at 12 days post-pollination and placed on wet ice for dissection. The kernels are cross sectioned laterally, dissecting just above the pedicel region, including 1-2 mm of the lower endosperm and the basal endosperm transfer region. The pedicel and lower endosperm region containing the basal endosperm transfer layer is pooled and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz049(Lib3088) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urbana, Illinois U.S.A) immature anther tissue from 8 weeks old plants. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Ears were harvested from 8 week old plants and were approximately 3.5-4.5 cm long. Kernels were dissected away from cob, frozen in liquid nitrogen and stored at -80C

until preparation of RNA. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz050 (Lib3114) cDNA library is generated from silks from maize (B73, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) plants at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is beyond the 10-leaf development stage and the ear shoots are approximately 15-20 cm in length. The ears are pulled and silks are separated from the ears and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON001 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) total leaf tissue at the V4 plant development stage. Leaf tissue from 38, field grown V4 stage plants is harvested from the 4th node. Leaf tissue is removed from the plants and immediately frozen in dry-ice. The harvested tissue is then

stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON002 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue at the V4 plant development stage. Root tissue from 76, field grown V4 stage plants is harvested. The root systems is cut from the soybean plant and washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON003 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling hypocotyl axis tissue harvested 2 day post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 2 days after the start of imbibition. The 2 days after imbibition samples are separated into 3 collections after removal of any adhering seed coat. At the 2 day stage, the hypocotyl axis is emerging from the soil. A few seedlings have cracked the soil surface and exhibited slight greening of the exposed cotyledons. The seedlings are washed in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON004 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling cotyledon tissue harvested 2 day post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 2 days after the start of imbibition. The 2 days after imbibition samples are separated into 3 collections after removal of any adhering seed coat. At the 2 day stage, the hypocotyl axis is emerging from the soil. A few seedlings have cracked the soil surface and exhibited slight greening of the exposed cotyledons. The seedlings are washed in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON005 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling hypocotyl axis tissue harvested 6 hour post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 6 hours after the start of imbibition. The 6 hours after imbibition samples are separated into 3 collections after removal of any adhering seed coat. The 6 hours after imbibition sample is collected over the course of approximately 2 hours starting at 6

hours post imbibition. At the 6 hours after imbibition stage, not all cotyledons have become fully hydrated and germination, or radicle protrusion, has not occurred. The seedlings are washed in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON006 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling cotyledons tissue harvested 6 hour post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 6 hours after imbibition. The 6 hours after imbibition samples are separated into 3 collections after removal of any adhering seed coat. The 6 hours after imbibition sample is collected over the course of approximately 2 hours starting at 6 hours post-imbibition. At the 6 hours after imbibition, not all cotyledons have become fully hydrated and germination or radicle protrusion, have not occurred. The seedlings are washed in water to remove soil, cotyledon harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON007 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 25 and 35 days post-flowering. Seed pods from field grown plants are harvested 25 and 35 days after flowering and

the seeds extracted from the pods. Approximately 4.4g and 19.3g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON008 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested from 25 and 35 days post-flowering plants. Total leaf tissue is harvested from field grown plants. Approximately 19g and 29g of leaves are harvested from the fourth node of the plant 25 and 35 days post-flowering and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON009 cDNA library is generated from soybean cutlivar C1944 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) pod and seed tissue harvested 15 days post-flowering. Pods from field grown plants are harvested 15 days post-flowering. Approximately 3g of pod tissue is harvested and immediately frozen in dry-ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON010 cDNA library is generated from soybean cultivar C1944 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) seed tissue harvested 40 days post-flowering. Pods from field grown plants are harvested 40 days post-flowering. Pods and seeds are separated, approximately 19g of seed tissue is harvested and immediately frozen in dry-ice.

The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON011 cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical germ plasma) leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON012 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue. Leaves from field grown plants are harvested from the fourth node 15 days post-flowering. Approximately 12g of leaves are harvested and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON013 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root and nodule tissue. Approximately, 28g of root tissue from field grown plants is harvested 15 days post-flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-

ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON014 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 25 and 35 days after flowering. Seed pods from field grown plants are harvested 15 days after flowering and the seeds extracted from the pods. Approximately 5g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON015 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 45 and 55 days post-flowering. Seed pods from field grown plants are harvested 45 and 55 days after flowering and the seeds extracted from the pods. Approximately 19g and 31g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON016 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue. Approximately, 61g and 38g of root tissue from field grown plants is harvested 25 and 35 days post- flowering is harvested. The root system is cut from the soybean plant and washed with water to free it from the soil. The tissue is placed in 14ml polystyrene tubes and immediately frozen in dry-ice. The harvested

tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON017 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue. Approximately 28g of root tissue from field grown plants is harvested 45 and 55 days post-flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON018 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested 45 and 55 days post-flowering. Leaves from field grown plants are harvested 45 and 55 days after flowering from the fourth node. Approximately 27g and 33g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON019 cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical germ plasma) root tissue. Roots are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are harvested from each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then

stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON020 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 65 and 75 days post-flowering. Seed pods from field grown plants are harvested 45 and 55 days after flowering and the seeds extracted from the pods. Approximately 14g and 31g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON021 cDNA library is generated from Soybean Cyst Nematode-resistant soybean cultivar Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) root tissue. Plants are grown in tissue culture at room temperature. At approximately 6 weeks post-germination, the plants are exposed to sterilized Soybean Cyst Nematode eggs. Infection is then allowed to progress for 10 days. After the 10 day infection process, the tissue is harvested. Agar from the culture medium and nematodes are removed and the root tissue is immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON022 (Lib3030) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) partially opened flower tissue. Partially to fully opened flower tissue is harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to

maintain even moisture conditions. A total of 3g of flower tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON023 cDNA library is generated from soybean genotype BW211S Null (Tohoku University, Morioka, Japan) seed tissue harvested 15 and 40 days post-flowering. Seed pods from field grown plants are harvested 15 and 40 days post-flowering and the seeds extracted from the pods. Approximately 0.7g and 14.2g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON024 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) internode-2 tissue harvested 18 days post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. The plants are grown in a greenhouse for 18 days after the start of imbibition at ambient temperature. Soil is checked and watered daily to maintain even moisture conditions. Stem tissue is harvested 18 days after the start of imbibition. The samples are divided into hypocotyl and internodes 1 through 5. The fifth internode contains some leaf bud material. Approximately 3 g of each sample is harvested and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON025 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested 65 days post-flowering.

Leaves are harvested from the fourth node of field grown plants 65 days post-flowering. Approximately 18.4g of leaf tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

SOYMON026 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue harvested 65 and 75 days post-flowering. Approximately 27g and 40g of root tissue from field grown plants is harvested 65 and 75 days post- flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON027 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) pod tissue, without seeds, harvested 25 days post-flowering. Seed pods from field grown plants are harvested 25 days post-flowering and the seeds extracted from the pods. Approximately 17g of seed pod tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at -80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON028 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought-stressed root tissue. The plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and

watered daily to maintain even moisture conditions. At the R3 stage of development, water is withheld from half of the plant collection (drought stressed population). After 3 days, half of the plants from the drought stressed condition and half of the plants from the control population are harvested. After another 3 days (6 days post drought induction) the remaining plants are harvested. A total of 27g and 40g of root tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON029 cDNA library is generated from Soybean Cyst Nematode-resistant soybean cultivar PI07354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) root tissue. Late fall to early winter greenhouse grown plants are exposed to Soybean Cyst Nematode eggs. At 10 days post-infection, the plants are uprooted, rinsed briefly and the roots frozen in liquid nitrogen. Approximately 20 grams of root tissue is harvested from the infected plants. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON030 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) flower bud tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Flower buds are removed from the plant at the pedicel. A total of 100mg of flower buds are harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA

preparation.Total RNA is prepared from 50 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA (Palo Alto, California (U.S.A.) library construction kit. The EcoRI/XhoI adaptors are used in this library construction. The cDNA is ligated into the pINCY vector.

The SOYMON031 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) carpel and stamen tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Flower buds are removed from the plant at the pedicel. Flowers are dissected to separate petals, sepals and reproductive structures (carpels and stamens). A total of 300mg of carpel and stamen tissue are harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. Total RNA is prepared from 150 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.) library construction kit. The EcoRI/XhoI adaptors are used in this library construction. The cDNA is ligated into the pINCY vector.

The SOYMON032 cDNA library is prepared from the Asgrow cultivar A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) rehydrated dry soybean seed meristem tissue. Surface sterilized seeds are germinated in liquid media for 24 hours. The seed axis is then excised from the barely germinating seed, placed on tissue culture media and incubated overnight at 20°C in the dark. The supportive tissue is removed from the explant prior to harvest.

Approximately 570mg of tissue is harvested and frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON033 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) heat-shocked seedling tissue without cotyledons. Seeds are imbibed and germinated in vermiculite for 2 days under constant illumination. After 48 hours, the seedlings are transferred to an incubator set at 40°C under constant illumination. After 30, 60 and 180 minutes seedlings are harvested and dissected. A portion of the seedling consisting of the root, hypocotyl and apical hook is frozen in liquid nitrogen and stored at −80°C. The seedlings after 2 days of imbibition are beginning to emerge from the vermiculite surface. The apical hooks are dark green in appearance. Total RNA and poly A^+ RNA is prepared from equal amounts of pooled tissue. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON034 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) cold-shocked seedling tissue without cotyledons. Seeds are imbibed and germinated in vermiculite for 2 days under constant illumination. After 48 hours, the seedlings are transferred to a cold room set at 5°C under constant illumination. After 30, 60 and 180 minutes seedlings are harvested and dissected. The seedlings after 2 days of imbibition are beginning to emerge from the vermiculite surface. The apical hooks are dark green in appearance. A portion of the seedling consisting of the root, hypocotyl and apical hook is frozen in liquid nitrogen and stored at −80°C. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON035 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed coat tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Seeds are harvested from mid to nearly full maturation (seed coats are not yellowing). The entire embryo proper is removed from the seed coat sample and the seed coat tissue are harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON036 cDNA library is generated from soybean cultivars PI171451, PI227687 and PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) insect challenged leaves. Plants from each of the three cultivars are grown in screenhouse conditions. The screenhouse is divided in half and one half of the screenhouse is infested with soybean looper and the other half infested with velvetbean caterpillar. A single leaf is taken from each of the representative plants at 3 different time points, 11 days after infestation, 2 weeks after infestation and 5 weeks after infestation and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. Total RNA and poly A+ RNA is isolated from pooled tissue consisting of equal quantities of all 18 samples (3 genotypes X 3 sample times X 2 insect genotypes). The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON037 cDNA library is generated from soybean cultivar A3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) etiolated axis and radical tissue. Seeds are planted in moist vermiculite, wrapped and kept at room temperature in complete darkness until harvest. Etiolated axis and hypocotyl tissue is harvested at 2, 3 and 4 days post-planting. A total of 1 gram of each tissue type is harvested at 2, 3 and 4 days after planting and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON038 cDNA library is generated from soybean variety Asgrow A3237 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) rehydrated dry seeds. Explants are prepared for transformation after germination of surface-sterilized seeds on solid tissue media. After 6days, at 28°C and 18 hours of light per day, the germinated seeds are cold shocked at 4°C for 24 hours. Meristemic tissue and part of the hypocotyl is remove and cotyledon excised. The prepared explant is then wounded for *Agrobacterium* infection. The 2 grams of harvested tissue is frozen in liquid nitrogen and stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy51 (LIB3027) normalized cDNA library is prepared from pooled seeds from SOYMON007, SOYMON015 and SOYMON020. Equal amounts of SOYMON007, SOYMON015, and SOYMON020 in the form of single stranded DNA, are mixed and used as the starting material for normalization. The normalized cDNA library is constructed as described in Example 2.

The Soy52 (LIB3028) normalized cDNA library is generated from flowers collected from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) plants. The

tissue descriptions for this library are identical to that for Soy35 (SOYMON022). The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The Soy53 (LIB3039) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling shoot apical meristem tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Apical tissue is harvested from seedling shoot meristem tissue, 7-8 days after the start of imbibition. The apex of each seedling is dissected to include the fifth node to the apical meristem. The fifth node corresponds to the third trifoliate leaf in the very early stages of development. Stipules completely envelop the leaf primordia at this time. A total of 200mg of apical tissue is harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy54 (LIB3040) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) heart to torpedo stage embryo tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Seeds are

collected and embryos removed from surrounding endosperm and maternal tissues. Embryos from globular to young torpedo stages (by corresponding analogy to *Arabidopsis*) are collected with a bias towards the middle of this spectrum. Embryos which are beginning to show asymmetric development of cotyledons are considered the upper developmental boundary for the collection and are excluded. A total of 12 mg embryo tissue is frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. Total RNA is prepared from 100 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.)) library construction kit. The SalI adaptors are used in this library construction. The cDNA is ligated into the pSPORT vector.

Soy55 (LIB3049) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) young seed tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Seeds are collected from very young pods (5 to 15 days after flowering). A total of 100mg of seeds are harvested and frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. Total RNA is prepared from 100 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.)) library construction kit. The SalI adaptors are used in this library construction. The cDNA is ligated into the pSPORT vector.

Soy56 (LIB3029) cDNA library is prepared from pooled seeds from Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020). Equal amounts of Soy19,

Soy27 and Soy33, in the form of single stranded DNA, are mixed in equimolar quantities. This mixture is used as a non-normalized control for comparison to Soy51. The cDNA library is constructed as described in Example 2.

TheSoy58 (LIB3050) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought stressed root tissue subtracted from control root tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of the plant drought is induced by withholding water. After 3 and 6 days root tissue from both drought stressed and control (watered regularly) plants are collected and frozen in dry-ice. The harvested tissue is stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2.

The Soy59 (LIB3051) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) endosperm tissue. Seeds are germinated on paper towels under laboratory ambient light conditions. At 8, 10 and 14 hours after imbibition, the seed coats are harvested. The endosperm consists of a very thin layer of tissue affixed to the inside of the seed coat. The seed coat and endosperm are frozen immediately after harvest in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed using the pSPORT cDNA

synthesis kit from Life Technologies (Life Technologies, Gaithersburg, Maryland U.S.A.). The resulting cDNA is ligated into the pSPORT.

The Soy60 (LIB3072) cDNA library is generated by subtracting the target cDNA, which is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seeds plus pods from drought stressed plants, from the driver cDNA, which is prepared from soybean cultivar Asgrow 3244 seeds plus pods from non drought-stressed (control) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 26°C and the nighttime temperature 21°C and 70% relative humidity. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of the plant drought is induced by withholding water. After 3 and 6 days seeds and pods from both drought stressed and control (watered regularly) plants are collected from the fifth and sixth node and frozen in dry-ice. The harvested tissue is stored at −80°C until RNA preparation. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2.

The Soy61 (LIB3073) cDNA library is generated by subtracting the target cDNA, which is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) jasmonic acid treated seedling, from the driver cDNA, which is prepared from control buffer treated seedlings without cotyledon. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to maintain even moisture conditions. At 9 days post

planting, the plantlets are sprayed with either control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean plantlets appear growth retarded. After 18 hours, 24 hours and 48 hours post treatment, the cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. To make RNA, the three sample timepoints were combined and ground. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2. For this library's construction, the eighth fraction of the cDNA size fractionation step was used for ligation.

The Soy62 (LIB3074) cDNA library is generated by subtracting the target cDNA, which is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) jasmonic acid treated seedlings without cotyledon, from the driver cDNA, which is prepared from soybean cultivar Asgrow 3244 control buffer treated seedlings without cotyledon.. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean plantlets appear growth retarded. After 18 hours, 24 hours and 48 hours post treatment, the

cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. To make RNA, the three sample timepoints were combined and ground. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2. For this library's construction, the ninth fraction of the cDNA size fractionation step was used for ligation.

The Soy65 (LIB3107) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) abscission zone tissue from drought-stressed plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Plants are irrigated with 15-16-17 Peter's Mix. At the R3 stage of development, drought is imposed by withholding water. At 3, 4, 5 and 6 days, tissue is harvested and wilting is not obvious until the fourth day. Abscission layers from reproductive organs are harvested by cutting less than one millimeter proximal and distal to the layer and immediately frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The following tissues are combined for the single library: four day stress, all nodes; 5 day stress, all nodes The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy66 (LIB3109) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) abscission zone tissue from control (watered regularly) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Plants are irrigated with 15-16-17 Peter's Mix. At 3, 4, 5 and 6 days (relative to drought stress induction in plants for soy65), abscission layer tissue is harvested. Abscission layers from reproductive organs are harvested by cutting less than one millimeter proximal and distal to the layer and immediately frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. The following samples are combined for this cDNA library: 4 day control, all nodes; 5 day control; all nodes. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

Soy67 (LIB3065) normalized cDNA library is prepared from pooled seeds from SOYMON007, SOYMON015 and SOYMON020 prepared tissue. Equal amounts of Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020), in the form of single stranded DNA, are mixed and used as the starting material for normalization. The normalized cDNA library is constructed as described in Example 2.

Soy68 (LIB3052) normalized cDNA library is prepared from pooled seeds from SOYMON007, SOYMON015 and SOYMON020. Equal amounts of Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020), in the form of single stranded DNA, are mixed and used as the starting material for normalization. The normalized cDNA library is constructed as described in Example 2.

Soy69 (LIB3053) normalized cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108

(Monsoy, Brazil) (tropical germ plasma) normalized leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

LIB3054 is a normalized cDNA library generated from roots from two exotic soybean cultivars Cristilliana and FT108 (Monsoy, Brazil, tropical germ plasma). The roots are harvested from plants grown an environmental chamber set to a 12h day/12h night cycle, 29°C daytime temperature, 24°C night temperature and 70% relative humidity. Daytime light levels are measured at 450µEinsteins/m^2. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are collected from each of the Cristilliana and FT108 cultivars. The plants are uprooted and the roots quickly rinsed in a pail of water. The root tissue is then cut from the plants, placed immediately in 14ml polystyrene tubes and immersed in dry-ice. The tissue is then transferred to a -80°C freezer for storage. Total RNA is prepared from the combination of equal amounts of root tissue from each cultivar. The RNA is prepared from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

Soy70 (LIB3055) cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical

germ plasma) leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

Soy71 (LIB3056) cDNA library is generated from soybean cultivars Cristalina and FT108 (tropical germ plasma) root tissue. Roots are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are harvested from each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3087 is a cDNA library that is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A). Seeds are imbibed in water for 4 hours at 30°C, and then the seed coat is removed. For the 4 hr timepoint, axis tissue is immediately harvested, and flash-frozen in liquid nitrogen. For 8 and 12 hr timepoints, decoated seeds are transferred to cotton saturated with water and incubated at 30°C for the remainder of the incubation period. Axis tissue is then excised and frozen in liquid nitrogen. Equal numbers of axes from each timepoint is pooled for RNA isolation. The collected tissue is stored at -80°C.

Axis tissue consists of unexpanded root, hypocotyl, epicotyl and apex. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3092 (Soy75) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought stressed leaf that is subtracted from a control. Seeds are planted in moist Metromix 350 medium at a depth of approximately 2cm. Trays are placed in an environmental chamber set to a 12h day/12h night cycle, 26°C daytime temperature, 21°C night temperature and 70% relative humidity. Daytime light levels are measured at 300mEinsteins/m^2. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of the plant, drought is induced by withholding water. After 3 and 6 days tissue is harvested. Leaves from both drought stressed and control (watered regularly) plants are collected from the fifth and sixth node and frozen in dry-ice. The tissue is then transferred to a -80°C freezer for storage. For subtraction, a standard cDNA library is constructed in the pSPORT vector. Driver first strand cDNA is covalently linked to Dynabeads following a protocol similar to that described in the Dynal literature. The target library is then heat denatured and hybridized to the driver cDNA in 400ml 4X SSPE for five rounds of hybridization at 68°C and 20 hours. After each hybridization, the hybridization solution is removed from the system and the hybridized target cDNA removed from the driver by heat denaturation in water. The refreshed driver is then reintroduced to the hybridization for the next round of hybridization. The remaining cDNA in the hybridization solution is then used to transform *E. coli* for sequencing.

Soy74 (LIB3093) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaves collected from control (watered regularly) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 26°C and the nighttime temperature 21°C and 70% relative humidity. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of the plant drought is induced by withholding water. After 3 and 6 days seeds and pods from both drought stressed and control (watered regularly) plants are collected from the fifth and sixth node and frozen in dry-ice. The harvested tissue from control plants is stored at −80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3094 is a normalized cDNA library that is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A). Seeds are imbibed in water for 4 hours at 30°C, and then the seed coat is removed. For the 4 hr timepoint, axis tissue is immediately harvested, and flash-frozen in liquid nitrogen. For 8 and 12 hr timepoints, decoated seeds are transferred to cotton saturated with water and incubated at 30°C for the remainder of the incubation period. Axis tissue is then excised and frozen in liquid nitrogen. Equal numbers of axes from each timepoint is pooled for RNA isolation. The collected tissue is stored at -80°C. Axis tissue consists of unexpanded root, hypocotyl, epicotyl and apex. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy76 (Lib3106) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) jasmonic acid and arachidonic treated seedlings. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to

maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean plantlets appear growth retarded. Arachidonic treated seedlings are sprayed with 1m/ml arachidonic acid in 0.1% Tween-20. After 18hours, 24hours and 48 hours post treatment, the cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. To make RNA, the three sample timepoints from the jasmonic acid treated seedlings are combined and ground. RNA from the arachidonic acid treated seedlings is isolated separately. Poly A^+ RNA is extracted from each total RNA sample separately and combined to make a cDNA library using approximately equal amounts of mRNA from each treatment. The cDNA library is constructed as described in Example 2. For the construction of this cDNA library, fraction 10 of the size fractionated cDNA is ligated into the pSPORT vector (Invitrogen, Carlsbad California U.S.A.) in order to capture some of the smaller transcripts characteristic of antifungal proteins.

Soy77 (LIB3108) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) control buffer (0.1% Tween-20) treated seedlings. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri

U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean plantlets appear growth retarded. After 18 hours, 24 hours and 48 hours post treatment, the cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. To make RNA, the three sample timepoints from control buffer treated seedlings are combined and ground. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2. For the construction of this cDNA library, fraction 10 of the size fractionated cDNA is ligated into the pSPORT vector in order to capture some of the smaller transcripts characteristic of antifungal proteins.

Soy72 (LIB3138) normalized cDNA library is generated from equal amounts of Soy5 (SOYMON001), Soy20 (SOYMON008) and Soy24 (SOYMON012), Soy28 (SOYMON018) and Soy38 (SOYMON025) in the form of double stranded DNA. These DNAs are mixed and used as the starting material for normalization. The tissue descriptions for these libraries are found above. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

Soy73 (LIB3139) normalized cDNA library is generated from equal amounts of Soy6 (SOYMON002), Soy25 (SOYMON013) and Soy29 (SOYMON016), Soy31 (SOYMON017) and Soy39 (SOYMON026) in the form of double stranded DNA. These DNAs are mixed and used as the starting material for normalization. The tissue descriptions for these libraries are found above. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

Example 2

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

Normalized libraries are made using essentially the Soares procedure (Soares *et al., Proc. Natl. Acad. Sci. (U.S.A.) 91*:9228-9232 (1994), the entirety of which is herein incorporated by reference). This approach is designed to reduce the initial 10,000-fold variation in individual cDNA frequencies to achieve abundances within one order of magnitude while maintaining the overall sequence complexity of the library. In the normalization process, the prevalence of high-abundance cDNA clones decreases dramatically, clones with mid-level abundance are relatively unaffected and clones for rare transcripts are effectively increased in abundance.

Normalized libraries are prepared from single-stranded and double-stranded DNA. Single-stranded and double-stranded DNA representing approximately 1 X 10^6 colony forming units are isolated using standard protocols. RNA, complementary to the single-stranded DNA, is synthesized using the double stranded DNA as a template. Biotinylated dATP is incorporated

into the RNA during the synthesis reaction. The single-stranded DNA is mixed with the biotinylated RNA in a 1:10 molar ratio) and allowed to hybridize. DNA-RNA hybrids are captured on Dynabeads M280 streptavidin (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.). The dynabeads with captured hybrids are collected with a magnet. The non-hybridized single-stranded molecules remaining after hybrid capture are converted to double stranded form and represent the primary normalized library.

For subtraction, target cDNA is made from the drought stressed tissue total RNA using the SMART cDNA synthesis system from Clonetech (Clonetech Laboratories, Palo Alto, California U.S.A.). Driver first strand cDNA is covalently linked to Dynabeads following a protocol similar to that described in the Dynal literature (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.). The target cDNA is then heat denatured and the second strand trapped using Dynabeads oligo-dT. The target second strand cDNA is then hybridized to the driver cDNA in 400μl 2X SSPE for two rounds of hybridization at 65°C and 20 hours. After each hybridization, the hybridization solution is removed from the system and the hybridized target cDNA removed from the driver by heat denaturation in water. After hybridization, the remaining cDNA is trapped with Dynabeads oligo-dT. The trapped cDNA is then amplified as in previous PCR based libraries and the resulting cDNA ligated into the pSPORT vector (Invitrogen, Carlsbad California U.S.A.).

Example 3

The cDNA libraries are plated on LB agar containing the appropriate antibiotics for selection and incubated at 37° for a sufficient time to allow the growth of individual colonies. Single colonies are individually placed in each well of a 96-well microtiter plates containing LB

liquid including the selective antibiotics. The plates are incubated overnight at approximately 37°C with gentle shaking to promote growth of the cultures. The plasmid DNA is isolated from each clone using Qiaprep plasmid isolation kits, using the conditions recommended by the manufacturer (Qiagen Inc., Santa Clara, California U.S.A.).

Template plasmid DNA clones are used for subsequent sequencing. For sequencing, the ABI PRISM dRhodamine Terminator Cycle Sequencing Ready Reaction Kit with AmpliTaq® DNA Polymerase, FS, is used (PE Applied Biosystems, Foster City, California U.S.A.).

Example 4

Nucleic acid sequences that encode for the following phosphogluconate pathway enzymes: glucose-6-phosphate-1-dehydrogenase; 6-phosphogluconate dehydrogenase; putative 6-phosphogluconate dehydrogenase; D-ribulose-5-phosphate-3-epimerase; ribose-5-phosphate isomerase; putative ribose-5-phosphate isomerase; transketolase; putative transketolase; transaldolase; putative transaldolase; and phosphoglucoisomerase; are identified from the Monsanto EST PhytoSeq database using TBLASTN (default values)(TBLASTN compares a protein query against the six reading frames of a nucleic acid sequence). Matches found with BLAST P values equal or less than 0.001 (probability) or BLAST Score of equal or greater than 90 are classified as hits. If the program used to determine the hit is HMMSW then the score refers to HMMSW score.

In addition, the GenBank database is searched with BLASTN and BLASTX (default values) using ESTs as queries. EST that pass the hit probability threshold of $10e^{-8}$ for the following enzymes are combined with the hits generated by using TBLASTN (described above) and classified by enzyme (see Table A below).

A cluster refers to a set of overlapping clones in the PhytoSeq database. Such an overlapping relationship among clones is designated as a "cluster" when BLAST scores from pairwise sequence comparisons of the member clones meets a predetermined minimum value or product score of 50 or more (Product Score = (BLAST SCORE x Percentage Identity)/(5 x minimum [length (Seq1), length (Seq2)])).

Since clusters are formed on the basis of single-linkage relationships, it is possible for two non-overlapping clones to be members of the same cluster if, for instance, they both overlap a third clone with at least the predetermined minimum BLAST score (stringency). A cluster ID is arbitrarily assigned to all of those clones which belong to the same cluster at a given stringency and a particular clone will belong to only one cluster at a given stringency. If a cluster contains only a single clone (a "singleton"), then the cluster ID number will be negative, with an absolute value equal to the clone ID number of its single member. Clones grouped in a cluster in most cases represent a contiguous sequence.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Nordine CHEIKH *et al.*

Appln. No.: To Be Assigned

Filed: April 28, 1999

For: Nucleic Acid Molecules and Other Molecules Associated with the Phosphogluconate Pathway

Art Unit: To Be Assigned

Examiner: To Be Assigned

Atty. Docket: 04983.0031.US01/ 38-21(15365)B

Statement Regarding Sequence Submission

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above-mentioned application are the same.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)

Date: April 28, 1999

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TABLE A*

PHOSPHOGLUCONATE PATHWAY ENZYMES

MAIZE GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
1	-700047645	700047645H1	SATMON003	g471345	BLASTX	193	1e-21	58
2	-700210379	700210379H1	SATMON016	g1480344	BLASTX	103	1e-10	85
3	9135	700203121H1	SATMON003	g1166405	BLASTX	108	1e-10	78

SOYBEAN GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
4	-700869140	700869140H1	SOYMON016	g2829880	BLASTX	164	1e-15	44
5	-701065174	701065174H1	SOYMON034	g603219	BLASTX	86	1e-9	76
6	-701130434	701130434H1	SOYMON037	g1197385	BLASTX	189	1e-19	55
7	-701149522	701149522H1	SOYMON031	g603219	BLASTX	99	1e-8	71
8	26484	701003905H1	SOYMON019	g1197385	BLASTX	138	1e-15	81
9	9136	701038169H1	SOYMON029	g603219	BLASTX	139	1e-21	73
10	9136	700903571H1	SOYMON022	g603219	BLASTX	144	1e-20	81
11	9136	701045122H1	SOYMON032	g603219	BLASTX	100	1e-13	79

MAIZE 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
12	-L30686779	LIB3068-060-Q1-K1-G12	LIB3068	g603221	BLASTX	186	1e-34	78
13	416	LIB3066-006-Q1-K1-H7	LIB3066	g2529228	BLASTN	865	1e-63	72
14	4882	LIB3059-023-Q1-K1-E8	LIB3059	g2529228	BLASTN	1058	1e-79	72
15	4882	LIB3069-050-Q1-K1-H6	LIB3069	g2529229	BLASTX	252	1e-69	83
16	4882	LIB3066-024-Q1-K1-G4	LIB3066	g2529229	BLASTX	256	1e-60	79
17	4882	LIB143-002-Q1-E1-A7	LIB143	g2529228	BLASTN	794	1e-57	74
18	4882	LIB3069-043-Q1-K1-E1	LIB3069	g2529228	BLASTN	749	1e-52	73
19	4882	LIB189-026-Q1-E1-G9	LIB189	g2529228	BLASTN	566	1e-36	75
20	4882	LIB3069-054-Q1-K1-H7	LIB3069	g2529228	BLASTN	510	1e-31	75
21	4882	LIB3062-033-Q1-K1-B9	LIB3062	g603221	BLASTX	151	1e-29	70

SOYBEAN 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
22	-700660509	700660509H1	SOYMON004	g2529228	BLASTN	641	1e-58	82
23	-700851941	700851941H1	SOYMON023	g2529228	BLASTN	363	1e-20	94
24	-700988668	700988668H1	SOYMON009	g2529228	BLASTN	221	1e-27	99
25	-701065575	701065575H1	SOYMON034	g2529228	BLASTN	375	1e-20	95
26	-701097417	701097417H1	SOYMON028	g2529228	BLASTN	229	1e-20	90

27	-701097624	701097624H1	SOYMON028	g2529228	BLASTN	596	1e-40	70
28	-701108654	701108654H1	SOYMON036	g2529228	BLASTN	817	1e-59	85
29	-701127281	701127281H1	SOYMON037	g2529228	BLASTN	209	1e-8	90
30	1015	701136806H1	SOYMON038	g2529228	BLASTN	1221	1e-92	96
31	1015	701135971H1	SOYMON038	g2529228	BLASTN	971	1e-72	92
32	1015	700996470H1	SOYMON018	g2529228	BLASTN	940	1e-71	95
33	1015	700737338H1	SOYMON010	g2529228	BLASTN	469	1e-30	91
34	12395	700900348H1	SOYMON027	g2529228	BLASTN	1313	1e-100	97
35	12395	701099109H1	SOYMON028	g2529228	BLASTN	1252	1e-95	98
36	12395	701138412H1	SOYMON038	g2529228	BLASTN	1205	1e-91	95
37	12395	700995812H1	SOYMON011	g2529228	BLASTN	863	1e-85	95
38	12395	701097095H1	SOYMON028	g2529228	BLASTN	641	1e-84	95
39	12395	700667386H1	SOYMON006	g2529228	BLASTN	1082	1e-81	96
40	14379	701098379H1	SOYMON028	g2529228	BLASTN	1258	1e-96	99
41	14379	700667507H1	SOYMON006	g2529228	BLASTN	764	1e-54	94
42	14813	700790407H2	SOYMON011	g2529228	BLASTN	726	1e-60	82
43	14813	700790454H2	SOYMON011	g2529228	BLASTN	297	1e-43	84
44	23322	701056256H1	SOYMON032	g2529228	BLASTN	1079	1e-99	97
45	23322	701006115H1	SOYMON019	g2529228	BLASTN	828	1e-97	97
46	23322	701046496H1	SOYMON032	g2529228	BLASTN	753	1e-71	91
47	23322	701127189H1	SOYMON037	g2529228	BLASTN	440	1e-42	94
48	23861	701123687H1	SOYMON037	g2529228	BLASTN	995	1e-81	93
49	23861	700562186H1	SOYMON002	g2529228	BLASTN	787	1e-56	95
50	25330	701155571H1	SOYMON031	g2529228	BLASTN	922	1e-86	95
51	25330	701151123H1	SOYMON031	g2529228	BLASTN	1147	1e-86	99
52	25330	700869362H1	SOYMON016	g2529228	BLASTN	569	1e-75	94
53	2704	700651490H1	SOYMON003	g2529228	BLASTN	1482	1e-126	98
54	2704	700746336H1	SOYMON013	g2529228	BLASTN	1221	1e-105	99
55	2704	701127584H1	SOYMON037	g2529228	BLASTN	973	1e-100	97
56	2704	701062890H1	SOYMON033	g2529228	BLASTN	1173	1e-99	97
57	2704	701070368H1	SOYMON034	g2529228	BLASTN	686	1e-97	95
58	2704	700848709H1	SOYMON021	g2529228	BLASTN	1277	1e-97	98
59	2704	700904479H1	SOYMON022	g2529228	BLASTN	1281	1e-97	99
60	2704	700748881H1	SOYMON013	g2529228	BLASTN	1264	1e-96	96
61	2704	700746110H1	SOYMON013	g2529228	BLASTN	1257	1e-95	97
62	2704	701036989H1	SOYMON029	g2529228	BLASTN	1090	1e-94	95
63	2704	700986972H1	SOYMON009	g2529228	BLASTN	1173	1e-93	96
64	2704	700832482H1	SOYMON019	g2529228	BLASTN	1202	1e-93	98
65	2704	701209853H1	SOYMON035	g2529228	BLASTN	1210	1e-92	97
66	2704	700981060H1	SOYMON009	g2529228	BLASTN	1198	1e-91	93
67	2704	700730187H1	SOYMON009	g2529228	BLASTN	1182	1e-89	99
68	2704	701010566H1	SOYMON019	g2529228	BLASTN	649	1e-88	90
69	2704	701008609H1	SOYMON019	g2529228	BLASTN	1124	1e-88	91
70	2704	700727312H1	SOYMON009	g2529228	BLASTN	1171	1e-88	94
71	2704	700750187H1	SOYMON013	g2529228	BLASTN	1059	1e-84	94
72	2704	700747389H1	SOYMON013	g2529228	BLASTN	614	1e-82	92
73	2704	700988527H1	SOYMON009	g2529228	BLASTN	781	1e-81	92
74	2704	700836168H1	SOYMON019	g2529228	BLASTN	1079	1e-81	93
75	2704	700904775H1	SOYMON022	g2529228	BLASTN	491	1e-80	95
76	2704	700566794H1	SOYMON002	g2529228	BLASTN	1045	1e-78	96
77	2704	700764571H1	SOYMON022	g2529228	BLASTN	1028	1e-76	91
78	2704	701047371H1	SOYMON032	g2529228	BLASTN	995	1e-74	96
79	2704	700727986H1	SOYMON009	g2529228	BLASTN	619	1e-73	92
80	2704	701009981H2	SOYMON019	g2529228	BLASTN	840	1e-71	93

81	2704	701049731H1	SOYMON032	g2529228	BLASTN	965	1e-71	98
82	2704	701105763H1	SOYMON036	g2529228	BLASTN	603	1e-70	92
83	2704	701214664H1	SOYMON035	g2529228	BLASTN	876	1e-64	93
84	2704	700889079H1	SOYMON024	g2529228	BLASTN	376	1e-43	92
85	2704	701037615H1	SOYMON029	g2529228	BLASTN	450	1e-28	85
86	502	700742139H1	SOYMON012	g2309076	BLASTX	179	1e-17	82
87	502	700743132H1	SOYMON012	g1573539	BLASTX	141	1e-12	87
88	6991	701048543H1	SOYMON032	g10409	BLASTX	116	1e-8	46
89	7306	700728579H1	SOYMON009	g2529228	BLASTN	797	1e-60	86
90	7306	700852657H1	SOYMON023	g2529228	BLASTN	739	1e-56	86
91	7306	700954712H1	SOYMON022	g2529228	BLASTN	700	1e-53	86
92	7306	700830929H1	SOYMON019	g2529228	BLASTN	693	1e-48	87
93	7306	700946027H1	SOYMON024	g2529228	BLASTN	681	1e-47	86
94	7306	701109643H1	SOYMON036	g2529228	BLASTN	566	1e-41	88
95	7306	700670024H1	SOYMON006	g2529228	BLASTN	478	1e-35	88
96	7306	700561367H1	SOYMON002	g2529228	BLASTN	274	1e-25	80
97	9847	700849887H1	SOYMON021	g2529228	BLASTN	246	1e-9	72
98	-GM11339	LIB3049-022-Q1-E1-H3	LIB3049	g2529228	BLASTN	1360	1e-111	86
99	14379	LIB3050-022-Q1-K1-H11	LIB3050	g2529228	BLASTN	1793	1e-143	96
100	14379	LIB3049-022-Q1-E1-H2	LIB3049	g2529228	BLASTN	1080	1e-137	97
101	16	LIB3040-004-Q1-E1-H4	LIB3040	g2529228	BLASTN	290	1e-36	96
102	23322	LIB3050-010-Q1-E1-D7	LIB3050	g2529228	BLASTN	726	1e-95	97
103	2704	LIB3039-020-Q1-E1-G6	LIB3039	g2529228	BLASTN	1060	1e-116	92

MAIZE PUTATIVE 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
104	-700159280	700159280H1	SATMON012	g3342801	BLASTN	677	1e-58	86
105	-700259383	700259383H1	SATMON017	g3342803	BLASTN	1210	1e-94	94
106	-700336103	700336103H1	SATMON019	g3342801	BLASTN	777	1e-93	96
107	-700347721	700347721H1	SATMON023	g3342799	BLASTN	282	1e-25	69
108	-700451974	700451974H1	SATMON028	g2529229	BLASTX	159	1e-15	60
109	-700549549	700549549H1	SATMON022	g3342799	BLASTN	1144	1e-86	86
110	-700570587	700570587H1	SATMON030	g3342801	BLASTN	780	1e-80	80
111	-701165285	701165285H1	SATMONN04	g3342801	BLASTN	469	1e-68	96
112	1485	700072738H1	SATMON007	g3342799	BLASTN	1670	1e-130	100
113	1485	700102916H1	SATMON010	g3342801	BLASTN	667	1e-107	97
114	1485	700075367H1	SATMON007	g3342799	BLASTN	1355	1e-104	100
115	1485	700215789H1	SATMON016	g3342799	BLASTN	1355	1e-104	100
116	1485	700618992H1	SATMON034	g3342799	BLASTN	926	1e-102	99
117	1485	700236444H1	SATMON010	g3342801	BLASTN	1237	1e-94	98
118	1485	701182383H1	SATMONN06	g3342801	BLASTN	707	1e-93	97
119	1485	700243716H1	SATMON010	g3342799	BLASTN	1233	1e-93	98
120	1485	700017132H1	SATMON001	g3342801	BLASTN	650	1e-84	100
121	1485	700000601H1	SATMON001	g3342801	BLASTN	1125	1e-84	100
122	1485	700000606H1	SATMON001	g3342801	BLASTN	1100	1e-82	100
123	1485	700473536H1	SATMON025	g3342799	BLASTN	1079	1e-81	97
124	1485	700000638H1	SATMON001	g3342801	BLASTN	1045	1e-78	100

125	1485	700000634H1	SATMON001	g3342801	BLASTN	1050	1e-78	100
126	1485	700000685H1	SATMON001	g3342801	BLASTN	1030	1e-77	100
127	1485	700620501H1	SATMON034	g3342801	BLASTN	834	1e-60	96
128	1485	700423115H1	SATMONN01	g3342801	BLASTN	718	1e-51	99
129	1485	700159096H1	SATMON012	g3342801	BLASTN	416	1e-48	84
130	1485	700450859H1	SATMON028	g3342799	BLASTN	414	1e-25	88
131	1485	700472336H1	SATMON025	g3342799	BLASTN	371	1e-22	90
132	17367	700615074H1	SATMON033	g3342802	BLASTX	120	1e-22	68
133	17367	700223083H1	SATMON011	g2529229	BLASTX	117	1e-18	58
134	20418	700142466H1	SATMON012	g3342801	BLASTN	586	1e-40	99
135	20418	700156495H1	SATMON012	g3342801	BLASTN	436	1e-27	97
136	416	700211273H1	SATMON016	g3342799	BLASTN	1536	1e-119	98
137	416	700085942H1	SATMON011	g3342799	BLASTN	1508	1e-116	99
138	416	700074747H1	SATMON007	g3342801	BLASTN	1018	1e-110	97
139	416	700572331H1	SATMON030	g3342799	BLASTN	1205	1e-108	98
140	416	700075257H1	SATMON007	g3342799	BLASTN	801	1e-105	98
141	416	700581966H1	SATMON031	g3342799	BLASTN	1330	1e-102	98
142	416	700220231H1	SATMON011	g3342801	BLASTN	1336	1e-102	99
143	416	700220126H1	SATMON011	g3342801	BLASTN	1327	1e-101	99
144	416	700238542H1	SATMON010	g3342801	BLASTN	1299	1e-99	98
145	416	700166459H1	SATMON013	g3342799	BLASTN	1217	1e-92	99
146	416	700221262H1	SATMON011	g3342801	BLASTN	1107	1e-83	90
147	416	700165558H1	SATMON013	g3342799	BLASTN	1061	1e-79	94
148	416	700449887H2	SATMON028	g3342799	BLASTN	986	1e-77	97
149	416	700460574H1	SATMON030	g3342799	BLASTN	702	1e-71	84
150	416	700220154H1	SATMON011	g3342801	BLASTN	917	1e-67	98
151	416	700614034H1	SATMON033	g3342799	BLASTN	666	1e-46	98
152	4839	700072438H2	SATMON007	g3342799	BLASTN	973	1e-103	96
153	4839	700021163H1	SATMON001	g3342799	BLASTN	853	1e-92	96
154	4839	700030139H1	SATMON003	g3342799	BLASTN	851	1e-91	98
155	4839	700021353H1	SATMON001	g3342799	BLASTN	866	1e-83	99
156	4839	700581184H1	SATMON031	g3342799	BLASTN	899	1e-73	95
157	4839	700219274H1	SATMON011	g3342801	BLASTN	518	1e-54	87
158	4839	700153705H1	SATMON007	g3342801	BLASTN	695	1e-52	87
159	4839	700341982H1	SATMON020	g3342799	BLASTN	360	1e-46	99
160	4839	700341234H1	SATMON020	g3342801	BLASTN	569	1e-38	89
161	4839	700343990H1	SATMON021	g3342799	BLASTN	366	1e-21	91
162	4882	700206482H1	SATMON003	g3342799	BLASTN	1592	1e-123	98
163	4882	700091812H1	SATMON011	g3342799	BLASTN	1546	1e-120	97
164	4882	700446652H1	SATMON027	g3342801	BLASTN	1455	1e-112	98
165	4882	700104823H1	SATMON010	g3342801	BLASTN	896	1e-111	98
166	4882	700356053H1	SATMON024	g3342801	BLASTN	1368	1e-105	97
167	4882	700219471H1	SATMON011	g3342801	BLASTN	920	1e-104	100
168	4882	700077133H1	SATMON007	g3342801	BLASTN	770	1e-102	97
169	4882	700208920H1	SATMON016	g3342801	BLASTN	701	1e-101	98
170	4882	700342808H1	SATMON021	g3342801	BLASTN	1170	1e-101	97
171	4882	700151209H1	SATMON007	g3342801	BLASTN	1321	1e-101	97
172	4882	700333146H1	SATMON019	g3342801	BLASTN	1011	1e-99	99
173	4882	700239943H1	SATMON010	g3342801	BLASTN	1295	1e-99	98
174	4882	700354623H1	SATMON024	g3342799	BLASTN	846	1e-98	98
175	4882	700348987H1	SATMON023	g3342801	BLASTN	997	1e-97	99
176	4882	700354655H1	SATMON024	g3342799	BLASTN	854	1e-94	96
177	4882	700075354H1	SATMON007	g3342801	BLASTN	1035	1e-93	100
178	4882	700351460H1	SATMON023	g3342801	BLASTN	946	1e-92	98

179	4882	700574482H1	SATMON030	g3342801	BLASTN	954	1e-92	97
180	4882	700455406H1	SATMON029	g3342801	BLASTN	663	1e-86	95
181	4882	700261343H1	SATMON017	g3342801	BLASTN	882	1e-81	93
182	4882	700156333H1	SATMON007	g3342801	BLASTN	1055	1e-79	100
183	4882	700152511H1	SATMON007	g3342801	BLASTN	786	1e-77	99
184	4882	700152557H1	SATMON007	g3342801	BLASTN	939	1e-74	97
185	4882	701176801H1	SATMONN05	g3342801	BLASTN	985	1e-73	100
186	4882	700242384H1	SATMON010	g3342801	BLASTN	676	1e-64	94
187	4882	700258317H1	SATMON017	g3342801	BLASTN	373	1e-61	98
188	4882	700377763H1	SATMON019	g3342801	BLASTN	615	1e-61	97
189	4882	700473877H1	SATMON025	g3342801	BLASTN	605	1e-46	100
190	4882	700076402H1	SATMON007	g3342801	BLASTN	256	1e-28	98
191	4882	700152333H1	SATMON007	g3342801	BLASTN	450	1e-28	100
192	4882	700155664H1	SATMON007	g3342801	BLASTN	260	1e-23	100
193	4882	700473648H1	SATMON025	g3342799	BLASTN	272	1e-16	91
194	4882	700548356H1	SATMON022	g3342799	BLASTN	290	1e-15	95
195	5830	700088306H1	SATMON011	g3342799	BLASTN	1604	1e-124	97
196	5830	700096066H1	SATMON008	g3342799	BLASTN	1575	1e-122	98
197	5830	700571406H1	SATMON030	g3342799	BLASTN	921	1e-118	96
198	5830	700075112H1	SATMON007	g3342799	BLASTN	1504	1e-116	95
199	5830	700050136H1	SATMON003	g3342799	BLASTN	1201	1e-91	97
200	5830	700028323H1	SATMON003	g3342799	BLASTN	1075	1e-90	97
201	5830	700076449H1	SATMON007	g3342799	BLASTN	1176	1e-89	94
202	5830	700352064H1	SATMON023	g3342799	BLASTN	1111	1e-86	96
203	5830	700346689H1	SATMON021	g3342799	BLASTN	1010	1e-75	96
204	5830	700217673H1	SATMON016	g3342799	BLASTN	1010	1e-75	97
205	5830	700350270H1	SATMON023	g3342799	BLASTN	405	1e-72	96
206	5830	700466829H1	SATMON025	g3342799	BLASTN	609	1e-50	96
207	5830	700220161H1	SATMON011	g3342799	BLASTN	590	1e-40	94
208	5830	700220192H1	SATMON011	g3342799	BLASTN	551	1e-37	96
209	5830	700453728H1	SATMON029	g3342799	BLASTN	491	1e-32	90

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Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
210	17920	700889178H1	SOYMON024	g3342801	BLASTN	480	1e-30	71
211	17920	700976950H1	SOYMON009	g3342801	BLASTN	303	1e-16	67
212	489	700744939H1	SOYMON013	g3342804	BLASTX	250	1e-29	79
213	489	700748139H1	SOYMON013	g3342800	BLASTX	150	1e-27	65
214	5856	701070317H1	SOYMON034	g3342800	BLASTX	132	1e-21	73

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Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
215	-700222465	700222465H1	SATMON011	g1162980	BLASTX	149	1e-27	84
216	-700618106	700618106H1	SATMON033	g902739	BLASTX	80	1e-25	76
217	10201	700101610H1	SATMON009	g902738	BLASTN	1009	1e-75	80
218	10201	700098237H1	SATMON009	g902738	BLASTN	1000	1e-74	80
219	10201	700209605H1	SATMON016	g1162979	BLASTN	976	1e-72	78
220	10201	700101988H1	SATMON009	g902738	BLASTN	626	1e-69	80
221	10201	700091966H1	SATMON011	g902738	BLASTN	905	1e-66	80
222	10201	700101445H1	SATMON009	g1162979	BLASTN	844	1e-61	80
223	10201	700159349H1	SATMON012	g902738	BLASTN	681	1e-48	73
224	10201	700380926H1	SATMON023	g902738	BLASTN	463	1e-45	81

225	17215	700048475H1	SATMON003	g1008313	BLASTX	177	1e-17	61
226	17215	700105805H1	SATMON010	g1008313	BLASTX	123	1e-10	59
227	1795	700432796H1	SATMONN01	g902739	BLASTX	139	1e-12	93
228	6043	700104089H1	SATMON010	g1162979	BLASTN	583	1e-39	79
229	6043	700099362H1	SATMON009	g1162980	BLASTX	156	1e-29	71
230	6043	700042321H1	SATMON004	g1162979	BLASTN	271	1e-27	79
231	6043	700457795H1	SATMON029	g902739	BLASTX	132	1e-25	64
232	6043	700096215H1	SATMON008	g1162980	BLASTX	120	1e-19	65
233	6043	700378379H1	SATMON019	g1162980	BLASTX	119	1e-17	86
234	6043	700239692H1	SATMON010	g1162980	BLASTX	167	1e-16	63
235	6043	700093535H1	SATMON008	g1162980	BLASTX	120	1e-13	61
236	6043	700098183H1	SATMON009	g1162980	BLASTX	121	1e-13	60
237	6043	700093175H1	SATMON008	g902739	BLASTX	126	1e-12	59
238	6043	700098056H1	SATMON009	g1162980	BLASTX	120	1e-9	57
239	6043	700101650H1	SATMON009	g1162980	BLASTX	120	1e-9	57
240	6043	700053356H1	SATMON009	g1162980	BLASTX	121	1e-9	57
241	6043	700099441H1	SATMON009	g902739	BLASTX	122	1e-9	58
242	7043	700162921H1	SATMON013	g1008313	BLASTX	130	1e-17	60
243	7043	700552657H1	SATMON022	g902739	BLASTX	154	1e-16	51
244	-L1891463	LIB189-001-Q1-E1-F4	LIB189	g1162979	BLASTN	596	1e-39	78
245	-L30781313	LIB3078-002-Q1-K1-A2	LIB3078	g1162979	BLASTN	440	1e-25	79
246	10201	LIB3078-034-Q1-K1-E8	LIB3078	g1162979	BLASTN	1271	1e-97	78
247	10201	LIB189-018-Q1-E1-G1	LIB189	g902738	BLASTN	1263	1e-96	79
248	10201	LIB3060-022-Q1-K1-G2	LIB3060	g902738	BLASTN	1228	1e-93	76
249	10201	LIB3060-034-Q1-K1-D3	LIB3060	g902738	BLASTN	1205	1e-91	79
250	10201	LIB36-007-Q1-E1-D10	LIB36	g1162979	BLASTN	989	1e-83	78
251	10201	LIB3078-053-Q1-K1-F4	LIB3078	g1162979	BLASTN	850	1e-62	68
252	10201	LIB189-034-Q1-E1-B12	LIB189	g902738	BLASTN	761	1e-53	74
253	1795	LIB3067-056-Q1-K1-A4	LIB3067	g902738	BLASTN	645	1e-43	80
254	6043	LIB189-017-Q1-E1-F12	LIB189	g1162979	BLASTN	842	1e-61	78
255	6043	LIB36-012-Q1-E1-H11	LIB36	g1162979	BLASTN	742	1e-51	78
256	6043	LIB3060-018-Q1-K1-B5	LIB3060	g1162979	BLASTN	653	1e-43	77
257	6043	LIB3062-015-Q1-K1-A11	LIB3062	g1162979	BLASTN	637	1e-42	77
258	6043	LIB189-031-Q1-E1-D1	LIB189	g1162979	BLASTN	532	1e-33	76
259	6043	LIB3060-013-Q1-K1-A2	LIB3060	g1162979	BLASTN	466	1e-27	75
260	7043	LIB148-032-Q1-E1-A4	LIB148	g2564973	BLASTX	238	1e-42	48

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Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
261	-700677209	700677209H1	SOYMON007	g1162980	BLASTX	130	1e-30	85
262	10469	700971857H1	SOYMON005	g1008313	BLASTX	208	1e-27	55
263	10469	701064495H1	SOYMON034	g1008313	BLASTX	208	1e-27	56
264	10469	701007767H1	SOYMON019	g1008313	BLASTX	129	1e-25	54
265	10469	700656367H1	SOYMON004	g1008313	BLASTX	182	1e-22	57
266	15209	700791582H1	SOYMON011	g2388956	BLASTX	129	1e-10	66
267	15209	701001180H1	SOYMON018	g1008313	BLASTX	122	1e-9	65
268	18337	700739263H1	SOYMON012	g902738	BLASTN	481	1e-50	82
269	18337	700681545H1	SOYMON008	g1162979	BLASTN	342	1e-44	83
270	18818	700866167H1	SOYMON016	g1162979	BLASTN	853	1e-62	89
271	18818	700983968H1	SOYMON009	g1162979	BLASTN	422	1e-55	76
272	5784	700999796H1	SOYMON018	g1162979	BLASTN	535	1e-43	78
273	5784	700788240H1	SOYMON011	g902738	BLASTN	455	1e-36	77
274	5784	701000905H1	SOYMON018	g902738	BLASTN	501	1e-36	77
275	5784	701040171H1	SOYMON029	g902738	BLASTN	510	1e-33	78
276	5784	700754807H1	SOYMON014	g902738	BLASTN	447	1e-31	72
277	5784	700904930H1	SOYMON022	g902738	BLASTN	465	1e-29	77
278	5784	700739828H1	SOYMON012	g902738	BLASTN	455	1e-28	76
279	5784	700741008H1	SOYMON012	g1162980	BLASTX	142	1e-16	81
280	5784	700738184H1	SOYMON012	g1162980	BLASTX	167	1e-16	81
281	5784	700790753H1	SOYMON011	g1162980	BLASTX	149	1e-15	79
282	5784	701110183H1	SOYMON036	g1162980	BLASTX	161	1e-15	81
283	5784	700876264H1	SOYMON018	g1162980	BLASTX	140	1e-12	87
284	5784	700787492H2	SOYMON011	g1162980	BLASTX	141	1e-12	76
285	5784	700788242H1	SOYMON011	g1162980	BLASTX	80	1e-11	89
286	5784	700741612H1	SOYMON012	g1162980	BLASTX	103	1e-11	78
287	5784	700789926H2	SOYMON011	g1162980	BLASTX	119	1e-11	74
288	5784	701105542H1	SOYMON036	g1162980	BLASTX	117	1e-10	66
289	5784	700741161H1	SOYMON012	g1162980	BLASTX	101	1e-8	63
290	5784	700877044H1	SOYMON018	g902738	BLASTN	236	1e-8	73
291	9624	700659817H1	SOYMON004	g1162979	BLASTN	959	1e-71	85
292	9624	700558457H1	SOYMON001	g1162979	BLASTN	533	1e-64	81
293	9624	700898624H1	SOYMON027	g1162979	BLASTN	867	1e-63	83
294	9624	700848716H1	SOYMON021	g1162979	BLASTN	680	1e-61	83
295	9624	700990488H1	SOYMON011	g1162979	BLASTN	763	1e-54	83
296	9624	700980873H1	SOYMON009	g1162979	BLASTN	722	1e-51	77
297	9624	700654880H1	SOYMON004	g1162979	BLASTN	473	1e-36	71
298	10469	LIB3040-057-Q1-E1-C5	LIB3040	g1008313	BLASTX	205	1e-60	54
299	9624	LIB3030-001-Q1-B1-F10	LIB3030	g1162979	BLASTN	1185	1e-90	80

MAIZE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
300	5053	700206243H1	SATMON003	g1669358	BLASTX	165	1e-20	59
301	5053	700157368H1	SATMON012	g1001678	BLASTX	188	1e-19	59
302	-L30672312	LIB3067-007-Q1-K1-C3	LIB3067	g1789280	BLASTX	114	1e-24	54
303	-L841459	LIB84-028-Q1-E1-A11	LIB84	g1789280	BLASTX	117	1e-25	53
304	5053	LIB3078-033-	LIB3078	g1001678	BLASTX	217	1e-42	50

		Q1-K1-A2						
305	5053	LIB3060-054-Q1-K1-G1	LIB3060	g2649655	BLASTX	100	1e-34	48
306	5053	LIB3078-054-Q1-K1-B9	LIB3078	g1669358	BLASTX	65	1e-24	40

SOYBEAN RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
307	17047	700737894H1	SOYMON012	g1001678	BLASTX	93	1e-14	62
308	17047	700790677H2	SOYMON011	g2649655	BLASTX	68	1e-9	47
309	17047	700891079H1	SOYMON024	g1001678	BLASTX	122	1e-9	56
310	8783	701120985H1	SOYMON037	g1789280	BLASTX	115	1e-9	51
311	8783	700745725H1	SOYMON013	g1789280	BLASTX	113	1e-8	51

MAIZE PUTATIVE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
312	-700622640	700622640H1	SATMON034	g3257798	BLASTX	128	1e-10	63
313	5053	700213140H1	SATMON016	g500774	BLASTX	195	1e-20	43

SOYBEAN PUTATIVE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
314	-700840778	700840778H1	SOYMON020	g500774	BLASTX	203	1e-21	51
315	-700898355	700898355H1	SOYMON027	g3257798	BLASTX	108	1e-17	60
316	16333	700562390H1	SOYMON002	g500774	BLASTX	211	1e-22	44
317	16333	700961206H1	SOYMON022	g500774	BLASTX	145	1e-14	51
318	8873	701120413H1	SOYMON037	g3257798	BLASTX	134	1e-11	48

MAIZE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
319	-700097383	700097383H1	SATMON009	g664902	BLASTN	1029	1e-76	80
320	-701159054	701159054H1	SATMONN04	g2529342	BLASTX	214	1e-27	79
321	-701184582	701184582H1	SATMONN06	g1658321	BLASTN	745	1e-53	74
322	1244	700553205H1	SATMON022	g1658321	BLASTN	816	1e-59	75
323	1244	700473792H1	SATMON025	g1658321	BLASTN	826	1e-59	75
324	1244	700405168H1	SATMON028	g1658321	BLASTN	805	1e-58	75
325	1244	700089307H1	SATMON011	g1658321	BLASTN	743	1e-53	74
326	1244	700355533H1	SATMON024	g1658321	BLASTN	589	1e-51	76
327	1244	700085136H1	SATMON011	g1658321	BLASTN	690	1e-48	76
328	1244	700382850H1	SATMON024	g664900	BLASTN	537	1e-47	72
329	1244	700454437H1	SATMON029	g1658321	BLASTN	655	1e-45	75
330	1244	700150022H1	SATMON007	g1658321	BLASTN	606	1e-41	76
331	1244	700212701H1	SATMON016	g1658321	BLASTN	507	1e-40	74
332	1244	700438654H1	SATMON026	g2529342	BLASTX	160	1e-24	89
333	1244	700458530H1	SATMON029	g2529342	BLASTX	177	1e-20	87
334	2946	700262031H1	SATMON017	g1658321	BLASTN	467	1e-30	74
335	3403	700075930H1	SATMON007	g664900	BLASTN	968	1e-71	81
336	3403	700381012H1	SATMON023	g1658321	BLASTN	949	1e-70	80
337	3403	700243701H1	SATMON010	g1658321	BLASTN	874	1e-63	80
338	3403	700220485H1	SATMON011	g664900	BLASTN	666	1e-54	74
339	3403	700045165H1	SATMON004	g664900	BLASTN	734	1e-52	73
340	3403	701185190H1	SATMONN06	g664900	BLASTN	709	1e-50	77

341	3403	700552475H1	SATMON022	g664900	BLASTN	591	1e-49	81
342	3403	700044755H1	SATMON004	g664900	BLASTN	690	1e-48	72
343	3403	700051910H1	SATMON003	g664900	BLASTN	671	1e-47	77
344	3403	700027425H1	SATMON003	g664900	BLASTN	675	1e-47	71
345	3403	700048347H1	SATMON003	g664900	BLASTN	662	1e-46	71
346	3403	700380608H1	SATMON021	g1658321	BLASTN	623	1e-43	82
347	3403	700448484H1	SATMON027	g664900	BLASTN	522	1e-33	71
348	3403	700184906H1	SATMON014	g2529342	BLASTX	251	1e-27	77
349	3403	700048819H1	SATMON003	g664900	BLASTN	453	1e-27	74
350	3403	701167994H1	SATMONN05	g2529342	BLASTX	193	1e-19	76
351	8097	700084375H1	SATMON011	g664900	BLASTN	855	1e-76	79
352	8097	700445226H1	SATMON027	g664900	BLASTN	464	1e-60	79
353	8097	700240770H1	SATMON010	g664900	BLASTN	750	1e-60	80
354	8097	700045122H1	SATMON004	g664900	BLASTN	638	1e-54	80
355	3403	LIB3060-013-Q1-K1-A12	LIB3060	g664900	BLASTN	1052	1e-78	72
356	3403	LIB3078-007-Q1-K1-G3	LIB3078	g664900	BLASTN	629	1e-41	69

SOYBEAN TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
357	-700646481	700646481H1	SOYMON013	g1658321	BLASTN	967	1e-71	83
358	-700734535	700734535H1	SOYMON010	g1658321	BLASTN	822	1e-59	82
359	-700865886	700865886H1	SOYMON016	g1658321	BLASTN	568	1e-38	82
360	-700943688	700943688H1	SOYMON024	g1658321	BLASTN	902	1e-66	82
361	-700954594	700954594H1	SOYMON022	g2529342	BLASTX	172	1e-16	75
362	-701064360	701064360H1	SOYMON034	g664901	BLASTX	179	1e-17	80
363	1039	700662776H1	SOYMON005	g1658321	BLASTN	755	1e-78	83
364	1039	700663764H1	SOYMON005	g1658321	BLASTN	839	1e-61	82
365	1039	700952282H1	SOYMON022	g1658321	BLASTN	785	1e-56	81
366	1039	700835426H1	SOYMON019	g1658321	BLASTN	748	1e-53	81
367	1039	700738038H1	SOYMON012	g1658321	BLASTN	559	1e-37	80
368	1040	700606230H1	SOYMON008	g1658321	BLASTN	532	1e-69	82
369	1040	700681196H2	SOYMON008	g1658321	BLASTN	866	1e-63	80
370	1040	700876408H1	SOYMON018	g1658321	BLASTN	475	1e-60	82
371	1040	700901259H1	SOYMON027	g1658321	BLASTN	821	1e-59	81
372	1040	700996991H1	SOYMON018	g1658321	BLASTN	450	1e-58	80
373	1040	700876984H1	SOYMON018	g1658321	BLASTN	807	1e-58	81
374	1040	700871885H1	SOYMON018	g1658321	BLASTN	812	1e-58	81
375	1040	700740158H1	SOYMON012	g1658321	BLASTN	767	1e-55	78
376	1040	700787592H1	SOYMON011	g1658321	BLASTN	770	1e-55	80
377	1040	700789355H2	SOYMON011	g1658321	BLASTN	727	1e-51	81
378	1040	700786173H2	SOYMON011	g1658321	BLASTN	523	1e-47	79
379	1040	700987027H1	SOYMON009	g1658321	BLASTN	680	1e-47	78
380	1040	700683335H1	SOYMON008	g1658321	BLASTN	567	1e-38	80
381	1040	700742402H1	SOYMON012	g1658321	BLASTN	521	1e-34	78
382	1040	700682934H1	SOYMON008	g1658322	BLASTX	111	1e-22	79
383	1040	701001535H1	SOYMON018	g664900	BLASTN	337	1e-18	85
384	1381	701002017H1	SOYMON018	g1658321	BLASTN	860	1e-62	81
385	1381	700680946H1	SOYMON008	g1658321	BLASTN	848	1e-61	75
386	1381	700785920H2	SOYMON011	g1658321	BLASTN	715	1e-60	80
387	1381	700741325H1	SOYMON012	g1658321	BLASTN	836	1e-60	81
388	1381	700737257H1	SOYMON010	g1658321	BLASTN	783	1e-56	83

389	1381	700743637H1	SOYMON012	g1658321	BLASTN	456	1e-47	79
390	1381	700683536H1	SOYMON008	g1658321	BLASTN	682	1e-47	82
391	1381	700899577H1	SOYMON027	g1658321	BLASTN	632	1e-43	73
392	1381	700655539H1	SOYMON004	g1658321	BLASTN	399	1e-32	77
393	1381	700743117H1	SOYMON012	g664901	BLASTX	144	1e-12	88
394	1381	701047167H1	SOYMON032	g1658321	BLASTN	147	1e-10	88
395	1694	700557862H1	SOYMON001	g1658321	BLASTN	918	1e-67	81
396	1694	701124388H1	SOYMON037	g1658321	BLASTN	884	1e-64	84
397	1694	700977906H1	SOYMON009	g1658321	BLASTN	741	1e-60	81
398	1694	700741633H1	SOYMON012	g1658321	BLASTN	753	1e-60	83
399	20534	701214424H1	SOYMON035	g1658321	BLASTN	855	1e-62	80
400	20534	701214345H1	SOYMON035	g1658321	BLASTN	845	1e-61	81
401	20534	700737144H1	SOYMON010	g1658321	BLASTN	743	1e-53	79
402	20534	700737045H1	SOYMON010	g1658321	BLASTN	716	1e-50	80
403	2081	700684191H1	SOYMON008	g1658321	BLASTN	243	1e-11	68
404	2081	700871634H1	SOYMON018	g1658321	BLASTN	243	1e-9	65
405	2081	700896859H1	SOYMON027	g1658321	BLASTN	243	1e-9	65
406	2081	700741968H1	SOYMON012	g1658321	BLASTN	243	1e-9	65
407	2081	700743285H1	SOYMON012	g1658321	BLASTN	234	1e-8	65
408	2081	701105794H1	SOYMON036	g1658321	BLASTN	236	1e-8	65
409	2081	700646243H1	SOYMON012	g1658321	BLASTN	236	1e-8	65
410	2081	701104160H1	SOYMON036	g1658321	BLASTN	236	1e-8	65
411	2081	700741863H1	SOYMON012	g1658321	BLASTN	238	1e-8	65
412	2091	700651076H1	SOYMON003	g1658321	BLASTN	1055	1e-79	79
413	2091	700874803H1	SOYMON018	g1658321	BLASTN	888	1e-65	82
414	2091	700988611H1	SOYMON009	g1658321	BLASTN	419	1e-61	79
415	2091	700657810H1	SOYMON004	g1658321	BLASTN	805	1e-58	81
416	2091	700739094H1	SOYMON012	g1658321	BLASTN	425	1e-54	82
417	2091	700962626H1	SOYMON022	g1658321	BLASTN	742	1e-52	78
418	2091	700990046H1	SOYMON011	g1658321	BLASTN	376	1e-34	79
419	3782	700870543H1	SOYMON018	g1658322	BLASTX	157	1e-25	68
420	4096	700556949H1	SOYMON001	g664901	BLASTX	188	1e-18	92
421	4096	700877014H1	SOYMON018	g664901	BLASTX	188	1e-18	92
422	4096	700877022H1	SOYMON018	g664901	BLASTX	188	1e-18	92
423	4096	700999039H1	SOYMON018	g664901	BLASTX	169	1e-16	91
424	7870	700998419H1	SOYMON018	g1658321	BLASTN	430	1e-51	80
425	7870	700557019H1	SOYMON001	g1658321	BLASTN	685	1e-48	80
426	7870	700786020H2	SOYMON011	g1658321	BLASTN	531	1e-41	78
427	7870	700740475H1	SOYMON012	g1658321	BLASTN	609	1e-41	74
428	7870	700875020H1	SOYMON018	g1658321	BLASTN	525	1e-34	79
429	7870	700674249H1	SOYMON007	g1658321	BLASTN	510	1e-33	82
430	7870	700658256H1	SOYMON004	g2529342	BLASTX	178	1e-22	61
431	7870	700677401H1	SOYMON007	g664901	BLASTX	158	1e-14	91
432	9031	700874020H1	SOYMON018	g1658321	BLASTN	789	1e-56	79
433	9031	700726463H1	SOYMON009	g1658321	BLASTN	758	1e-54	76
434	9031	700869017H1	SOYMON016	g664900	BLASTN	743	1e-53	77
435	9031	700566216H1	SOYMON002	g664901	BLASTX	201	1e-20	92
436	1039	LIB3051-053-Q1-K2-F1	LIB3051	g1658321	BLASTN	1326	1e-101	80
437	9031	LIB3039-045-Q1-E1-D1	LIB3039	g1658321	BLASTN	1033	1e-77	79

MAIZE PUTATIVE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
438	-700045462	700045462H1	SATMON004	g2612940	BLASTN	1219	1e-92	89
439	-700223919	700223919H1	SATMON011	g2612940	BLASTN	1025	1e-76	87
440	-700256830	700256830H1	SATMON017	g2612940	BLASTN	1029	1e-76	87
441	-701169515	701169515H1	SATMONN05	g2612940	BLASTN	327	1e-40	92
442	23377	700263420H1	SATMON017	g2612940	BLASTN	489	1e-31	75
443	23377	701185311H1	SATMONN06	g2612940	BLASTN	460	1e-27	78
444	7446	700624329H1	SATMON034	g2612940	BLASTN	1046	1e-87	88
445	7446	700159091H1	SATMON012	g2612940	BLASTN	898	1e-77	89
446	-L30626416	LIB3062-048-Q1-K1-D12	LIB3062	g2612940	BLASTN	808	1e-74	86
447	-L30684293	LIB3068-046-Q1-K1-B2	LIB3068	g2612940	BLASTN	846	1e-90	87

SOYBEAN PUTATIVE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
448	19183	700907766H1	SOYMON022	g2612940	BLASTN	395	1e-30	68
449	-700764341	700764341H1	SOYMON021	g2612941	BLASTX	247	1e-39	75
450	-700888745	700888745H1	SOYMON024	g2612941	BLASTX	237	1e-27	76
451	-700909473	700909473H1	SOYMON022	g2612941	BLASTX	114	1e-16	53
452	7224	700681472H2	SOYMON008	g2612941	BLASTX	107	1e-12	72
453	19325	700751059H1	SOYMON014	g2244912	BLASTX	160	1e-15	78

MAIZE TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
454	-700074081	700074081H1	SATMON007	g2078350	BLASTX	199	1e-26	79
455	-700087740	700087740H1	SATMON011	g2078349	BLASTN	651	1e-45	68
456	10709	700049020H1	SATMON003	g2078350	BLASTX	131	1e-10	67
457	143	700207653H1	SATMON016	g2078349	BLASTN	911	1e-67	76
458	143	700099852H1	SATMON009	g2078349	BLASTN	889	1e-65	75
459	143	700268119H1	SATMON017	g2078349	BLASTN	872	1e-63	76
460	143	700211193H1	SATMON016	g2078349	BLASTN	848	1e-61	76
461	143	700454251H1	SATMON029	g2078349	BLASTN	829	1e-60	78
462	143	700204216H1	SATMON003	g2078349	BLASTN	801	1e-57	76
463	143	700333262H1	SATMON019	g2078349	BLASTN	691	1e-56	74
464	143	700618845H1	SATMON034	g2078349	BLASTN	781	1e-56	76
465	143	700239238H1	SATMON010	g2078349	BLASTN	776	1e-55	76
466	143	700205539H1	SATMON003	g2078349	BLASTN	754	1e-54	73
467	143	700344192H1	SATMON021	g2078349	BLASTN	756	1e-54	75
468	143	700239126H1	SATMON010	g2078349	BLASTN	733	1e-52	73
469	143	700207418H1	SATMON016	g2078349	BLASTN	736	1e-52	70
470	143	700575204H1	SATMON030	g2078349	BLASTN	741	1e-52	71
471	143	700442682H1	SATMON026	g2078349	BLASTN	725	1e-51	74
472	143	700343686H1	SATMON021	g2078349	BLASTN	556	1e-49	74
473	143	700241386H1	SATMON010	g2078349	BLASTN	694	1e-49	75
474	143	700209193H1	SATMON016	g2078349	BLASTN	704	1e-49	72
475	143	700549360H1	SATMON022	g2078349	BLASTN	689	1e-48	77
476	143	700213668H1	SATMON016	g2078349	BLASTN	690	1e-48	72
477	143	700099381H1	SATMON009	g2078349	BLASTN	691	1e-48	73
478	143	700241472H1	SATMON010	g2078349	BLASTN	507	1e-47	76
479	143	700158253H1	SATMON012	g2078349	BLASTN	670	1e-47	76

480	143	700243043H1	SATMON010	g2078349	BLASTN	680	1e-47	73
481	143	700077153H1	SATMON007	g2078350	BLASTX	238	1e-46	74
482	143	700094547H1	SATMON008	g2078349	BLASTN	659	1e-46	73
483	143	700237891H1	SATMON010	g2078349	BLASTN	638	1e-44	71
484	143	700142446H1	SATMON012	g2078349	BLASTN	625	1e-43	75
485	143	700440545H1	SATMON026	g2078349	BLASTN	626	1e-43	71
486	143	700622336H1	SATMON034	g2078349	BLASTN	633	1e-43	72
487	143	700082380H1	SATMON011	g2078349	BLASTN	610	1e-42	70
488	143	700171422H1	SATMON013	g2078349	BLASTN	602	1e-41	77
489	143	700449973H1	SATMON028	g2078349	BLASTN	609	1e-41	70
490	143	701182293H1	SATMONN06	g2078349	BLASTN	480	1e-40	72
491	143	700154086H1	SATMON007	g2078349	BLASTN	592	1e-40	71
492	143	700018427H1	SATMON001	g2078349	BLASTN	593	1e-40	78
493	143	700615631H1	SATMON033	g2078349	BLASTN	608	1e-40	71
494	143	700550235H1	SATMON022	g2078350	BLASTX	237	1e-38	78
495	143	700203959H1	SATMON003	g2078349	BLASTN	571	1e-38	73
496	143	700152039H1	SATMON007	g2078349	BLASTN	532	1e-35	72
497	143	700207472H1	SATMON016	g2078350	BLASTX	168	1e-34	67
498	143	700580755H1	SATMON031	g2078350	BLASTX	202	1e-33	73
499	143	700477590H1	SATMON025	g2078349	BLASTN	365	1e-32	74
500	143	700083979H1	SATMON011	g2078349	BLASTN	517	1e-32	70
501	143	700569751H1	SATMON030	g2078350	BLASTX	161	1e-30	63
502	143	700239239H1	SATMON010	g2078350	BLASTX	182	1e-30	69
503	143	700469525H1	SATMON025	g2078350	BLASTX	270	1e-30	64
504	143	700242890H1	SATMON010	g2078349	BLASTN	451	1e-28	71
505	143	700168126H1	SATMON013	g2078349	BLASTN	448	1e-27	71
506	143	700338361H1	SATMON020	g2078349	BLASTN	441	1e-26	72
507	143	700337834H1	SATMON020	g2078349	BLASTN	444	1e-26	73
508	143	700339742H1	SATMON020	g2078349	BLASTN	434	1e-25	71
509	143	700205161H1	SATMON003	g2078350	BLASTX	171	1e-22	69
510	143	700171567H1	SATMON013	g2078350	BLASTX	212	1e-21	86
511	143	700202495H1	SATMON003	g2078350	BLASTX	195	1e-19	80
512	143	700266495H1	SATMON017	g2078350	BLASTX	175	1e-16	73
513	143	701173375H2	SATMONN05	g2078350	BLASTX	112	1e-13	78
514	143	700404964H1	SATMON027	g2078350	BLASTX	133	1e-11	77
515	143	700430542H1	SATMONN01	g2078350	BLASTX	137	1e-11	77
516	143	701181429H1	SATMONN06	g2078349	BLASTN	238	1e-8	74
517	14658	700622708H1	SATMON034	g4602	BLASTX	144	1e-20	40
518	14658	700196413H1	SATMON014	g1574680	BLASTX	118	1e-9	43
519	15681	700261694H1	SATMON017	g4602	BLASTX	80	1e-10	35
520	143	LIB3062-030-Q1-K1-A8	LIB3062	g2078349	BLASTN	878	1e-80	74
521	143	LIB3060-017-Q1-K1-G11	LIB3060	g2078349	BLASTN	1041	1e-77	73
522	143	LIB3060-002-Q1-K2-A11	LIB3060	g2078349	BLASTN	1009	1e-75	73
523	143	LIB3069-030-Q1-K1-A11	LIB3069	g2078349	BLASTN	877	1e-68	71
524	143	LIB3060-032-Q1-K1-C7	LIB3060	g2078349	BLASTN	660	1e-66	72
525	143	LIB3059-017-Q1-K1-B4	LIB3059	g2078349	BLASTN	885	1e-64	73
526	143	LIB3066-053-Q1-K1-G10	LIB3066	g2078349	BLASTN	833	1e-60	69

527	143	LIB3060-017-Q1-K1-G12	LIB3060	g2078349	BLASTN	756	1e-53	73
528	143	LIB143-027-Q1-E1-B11	LIB143	g2078350	BLASTX	246	1e-42	75
529	143	LIB3059-016-Q1-K1-H12	LIB3059	g2078350	BLASTX	138	1e-36	59
530	15681	LIB3062-027-Q1-K1-H4	LIB3062	g1786189	BLASTX	112	1e-32	42
531	19642	LIB143-006-Q1-E1-H7	LIB143	g1574680	BLASTX	91	1e-26	41
532	29728	LIB3079-007-Q1-K1-G3	LIB3079	g2078350	BLASTX	238	1e-41	68
533	29728	LIB3069-033-Q1-K1-E2	LIB3069	g2078350	BLASTX	96	1e-25	65

SOYBEAN TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
534	-700557848	700557848H1	SOYMON001	g1786189	BLASTX	138	1e-12	62
535	-700898220	700898220H1	SOYMON027	g2078350	BLASTX	96	1e-13	79
536	-701053141	701053141H1	SOYMON032	g2078350	BLASTX	190	1e-24	63
537	12032	701209342H1	SOYMON035	g2078349	BLASTN	882	1e-64	79
538	12032	700566011H1	SOYMON002	g2078349	BLASTN	521	1e-43	79
539	12032	700957709H1	SOYMON022	g2078349	BLASTN	607	1e-41	72
540	16286	701014315H1	SOYMON019	g2078349	BLASTN	632	1e-43	75
541	16286	700733731H1	SOYMON010	g2078350	BLASTX	171	1e-27	64
542	16286	700978907H1	SOYMON009	g2078349	BLASTN	452	1e-27	75
543	16286	700675063H1	SOYMON007	g2078350	BLASTX	159	1e-23	66
544	18022	700963175H1	SOYMON022	g2078349	BLASTN	771	1e-55	80
545	18022	700892251H1	SOYMON024	g2078349	BLASTN	519	1e-34	81
546	18700	700741418H1	SOYMON012	g2078349	BLASTN	440	1e-26	75
547	18700	701210709H1	SOYMON035	g2078350	BLASTX	227	1e-24	90
548	18700	700867261H1	SOYMON016	g2078350	BLASTX	158	1e-14	85
549	18700	700867361H1	SOYMON016	g2078349	BLASTN	179	1e-11	79
550	3993	700893136H1	SOYMON024	g2078349	BLASTN	725	1e-51	78
551	3993	700747125H1	SOYMON013	g2078349	BLASTN	613	1e-49	79
552	3993	701044349H1	SOYMON032	g2078349	BLASTN	630	1e-43	74
553	3993	700832771H1	SOYMON019	g2078349	BLASTN	608	1e-41	74
554	3993	700975359H1	SOYMON009	g2078349	BLASTN	449	1e-28	71
555	3993	700970463H1	SOYMON005	g2078350	BLASTX	83	1e-22	74
556	3993	701012833H1	SOYMON019	g2078350	BLASTX	207	1e-21	52
557	3993	700794982H1	SOYMON017	g2078349	BLASTN	335	1e-19	75
558	3993	701012461H1	SOYMON019	g2078350	BLASTX	189	1e-18	50
559	3993	700982758H1	SOYMON009	g2078349	BLASTN	337	1e-17	75
560	3993	701102424H1	SOYMON028	g2078350	BLASTX	161	1e-15	70
561	3993	700746415H1	SOYMON013	g2078349	BLASTN	320	1e-15	74
562	3993	700897055H1	SOYMON027	g2078349	BLASTN	289	1e-13	73
563	3993	700967006H1	SOYMON029	g2078349	BLASTN	289	1e-13	73
564	3993	701100750H1	SOYMON028	g2078349	BLASTN	182	1e-12	78
565	3993	701055410H1	SOYMON032	g2078350	BLASTX	120	1e-11	60
566	3993	701040696H1	SOYMON029	g2078349	BLASTN	263	1e-11	72
567	3993	701211427H1	SOYMON035	g2078350	BLASTX	73	1e-10	50
568	3993	700963010H1	SOYMON022	g2078350	BLASTX	73	1e-10	50
569	3993	701099581H1	SOYMON028	g2078350	BLASTX	97	1e-10	50

570	3993	700888568H1	SOYMON024	g2078350	BLASTX	112	1e-10	47
571	3993	701011889H1	SOYMON019	g2078350	BLASTX	124	1e-10	48
572	3993	700726386H1	SOYMON009	g2078350	BLASTX	90	1e-9	48
573	3993	700943367H1	SOYMON024	g2078349	BLASTN	242	1e-9	72
574	3993	700650311H1	SOYMON003	g2078349	BLASTN	242	1e-9	72
575	3993	701008074H1	SOYMON019	g2078350	BLASTX	83	1e-8	48
576	3993	700955316H1	SOYMON022	g2078349	BLASTN	155	1e-8	72
577	3993	701043442H1	SOYMON029	g2078349	BLASTN	234	1e-8	73
578	3993	700905939H1	SOYMON022	g2078349	BLASTN	234	1e-8	73
579	3993	700728911H1	SOYMON009	g2078349	BLASTN	234	1e-8	73
580	4079	700565922H1	SOYMON002	g2078349	BLASTN	574	1e-72	83
581	4079	700991339H1	SOYMON011	g2078349	BLASTN	918	1e-67	81
582	4079	700746817H1	SOYMON013	g2078349	BLASTN	902	1e-66	81
583	4079	701007939H1	SOYMON019	g2078349	BLASTN	877	1e-64	80
584	4079	701015475H1	SOYMON019	g2078349	BLASTN	843	1e-61	82
585	4079	701097904H1	SOYMON028	g2078349	BLASTN	826	1e-60	81
586	4079	700744275H1	SOYMON013	g2078349	BLASTN	833	1e-60	80
587	4079	700907055H1	SOYMON022	g2078349	BLASTN	624	1e-59	82
588	4079	701102453H1	SOYMON028	g2078349	BLASTN	453	1e-58	80
589	4079	700795760H1	SOYMON017	g2078349	BLASTN	804	1e-58	80
590	4079	700837515H1	SOYMON020	g2078349	BLASTN	811	1e-58	84
591	4079	700943689H1	SOYMON024	g2078349	BLASTN	782	1e-56	81
592	4079	701009626H1	SOYMON019	g2078349	BLASTN	715	1e-55	85
593	4079	700978865H1	SOYMON009	g2078349	BLASTN	334	1e-51	81
594	4079	700731620H1	SOYMON010	g2078349	BLASTN	400	1e-51	79
595	4079	700891691H1	SOYMON024	g2078349	BLASTN	713	1e-50	80
596	4079	700957819H1	SOYMON022	g2078349	BLASTN	677	1e-47	79
597	4079	700563553H1	SOYMON002	g2078349	BLASTN	547	1e-46	77
598	4079	700846208H1	SOYMON021	g2078349	BLASTN	524	1e-45	79
599	4079	700965218H1	SOYMON022	g2078349	BLASTN	622	1e-43	80
600	4079	700897435H1	SOYMON027	g2078349	BLASTN	633	1e-43	80
601	-GM20444	LIB3056-010-Q1-N1-B6	LIB3056	g2078349	BLASTN	837	1e-71	74
602	12032	LIB3056-013-Q1-N1-E12	LIB3056	g2078349	BLASTN	722	1e-94	78
603	16286	LIB3029-008-Q1-B1-B11	LIB3029	g2078349	BLASTN	1047	1e-78	74
604	18700	LIB3051-043-Q1-K1-C2	LIB3051	g2078349	BLASTN	626	1e-41	75
605	3993	LIB3051-038-Q1-K1-G6	LIB3051	g2078349	BLASTN	651	1e-56	75
606	3993	LIB3051-077-Q1-K1-B8	LIB3051	g2078349	BLASTN	807	1e-56	75
607	3993	LIB3051-115-Q1-K1-B3	LIB3051	g2078349	BLASTN	511	1e-54	75
608	3993	LIB3051-054-Q1-K2-C5	LIB3051	g2078349	BLASTN	755	1e-52	75
609	3993	LIB3040-029-Q1-E1-B10	LIB3040	g2078350	BLASTX	117	1e-43	61
610	3993	LIB3040-059-Q1-E1-F9	LIB3040	g2078350	BLASTX	217	1e-42	57
611	3993	LIB3051-087-Q1-K1-A8	LIB3051	g2078349	BLASTN	368	1e-38	75
612	3993	LIB3056-001-	LIB3056	g2078349	BLASTN	520	1e-32	72

		Q1-B1-C11						
613	3993	LIB3051-112-Q1-K1-H9	LIB3051	g2078349	BLASTN	393	1e-30	71
614	4079	LIB3056-008-Q1-N1-H10	LIB3056	g2078349	BLASTN	1357	1e-104	81
615	4079	LIB3050-022-Q1-K1-B11	LIB3050	g2078349	BLASTN	1338	1e-102	81
616	4079	LIB3051-094-Q1-K1-B8	LIB3051	g2078349	BLASTN	1088	1e-81	80
617	4079	LIB3050-021-Q1-K1-G2	LIB3050	g2078349	BLASTN	673	1e-49	77

MAIZE PUTATIVE TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
618	15681	700429804H1	SATMONN01	g1323043	BLASTX	100	1e-11	37

MAIZE PHOSPHOGLUCOISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
619	-700086021	700086021H1	SATMON011	g1100771	BLASTX	225	1e-28	51
620	-700169489	700169489H1	SATMON013	g1100771	BLASTX	152	1e-13	59
621	-700222638	700222638H1	SATMON011	g1100771	BLASTX	256	1e-28	60
622	-700445574	700445574H1	SATMON027	g1100771	BLASTX	143	1e-12	54
623	-700475232	700475232H1	SATMON025	g596022	BLASTN	845	1e-61	90
624	-700612774	700612774H1	SATMON033	g596022	BLASTN	1574	1e-122	95
625	14393	700222547H1	SATMON011	g1100771	BLASTX	239	1e-25	60
626	14393	700220357H1	SATMON011	g1100771	BLASTX	218	1e-23	68
627	14393	700050317H1	SATMON003	g1100771	BLASTX	120	1e-22	63
628	14393	700163544H1	SATMON013	g1100771	BLASTX	214	1e-22	62
629	15724	700207164H1	SATMON017	g1100771	BLASTX	135	1e-17	67
630	15724	700552402H1	SATMON022	g1100771	BLASTX	135	1e-11	60
631	15724	700086085H1	SATMON011	g1100771	BLASTX	137	1e-11	45
632	20643	700577051H1	SATMON031	g1100771	BLASTX	241	1e-26	66
633	20643	700201592H1	SATMON003	g1100771	BLASTX	113	1e-19	45
634	20643	700576644H1	SATMON030	g1100771	BLASTX	113	1e-17	43
635	2351	700208928H1	SATMON016	g1100771	BLASTX	274	1e-43	73
636	2351	700240758H1	SATMON010	g1100771	BLASTX	283	1e-43	79
637	2351	700352502H1	SATMON023	g1100771	BLASTX	197	1e-36	70
638	2351	700581930H1	SATMON031	g1100771	BLASTX	164	1e-34	72
639	2351	700028642H1	SATMON003	g1100771	BLASTX	294	1e-33	65
640	2351	700106092H1	SATMON010	g1100771	BLASTX	294	1e-33	62
641	2351	700082102H1	SATMON011	g1100771	BLASTX	300	1e-33	62
642	2351	700083446H1	SATMON011	g1100771	BLASTX	274	1e-30	65
643	2351	700580585H1	SATMON031	g1100771	BLASTX	163	1e-29	69
644	2351	700550608H1	SATMON022	g1100771	BLASTX	265	1e-29	61
645	2351	700106079H1	SATMON010	g1100771	BLASTX	261	1e-28	54
646	2351	700244248H1	SATMON010	g1100771	BLASTX	238	1e-25	67
647	2351	700152233H1	SATMON007	g1100771	BLASTX	167	1e-22	72
648	2351	700455043H1	SATMON029	g1100771	BLASTX	168	1e-21	68
649	2351	700615809H1	SATMON033	g1100771	BLASTX	207	1e-21	66
650	2351	701165320H1	SATMONN04	g1100771	BLASTX	122	1e-14	63
651	32930	700042996H1	SATMON004	g596022	BLASTN	476	1e-95	98
652	4222	700222539H1	SATMON011	g596022	BLASTN	1160	1e-87	100

653	4222	700104023H1	SATMON010	g596022	BLASTN	1060	1e-84	100
654	4222	700101580H1	SATMON009	g596022	BLASTN	871	1e-74	99
655	4222	700473395H1	SATMON025	g596022	BLASTN	368	1e-46	95
656	4222	700800179H1	SATMON036	g596022	BLASTN	240	1e-11	100
657	8858	700221523H1	SATMON011	g1100771	BLASTX	278	1e-31	59
658	895	700100965H1	SATMON009	g596022	BLASTN	1611	1e-125	99
659	895	700620985H1	SATMON034	g596022	BLASTN	1418	1e-114	98
660	895	700082062H1	SATMON011	g596022	BLASTN	1365	1e-110	97
661	895	700573782H1	SATMON030	g596022	BLASTN	920	1e-107	98
662	895	700236138H1	SATMON010	g596022	BLASTN	1395	1e-107	100
663	895	700086336H1	SATMON011	g596022	BLASTN	1370	1e-105	100
664	895	700801467H1	SATMON036	g596022	BLASTN	1249	1e-99	95
665	895	700801458H1	SATMON036	g596022	BLASTN	1245	1e-98	100
666	895	700475024H1	SATMON025	g596022	BLASTN	1162	1e-97	93
667	895	700243164H1	SATMON010	g596022	BLASTN	1105	1e-96	100
668	895	700804665H1	SATMON036	g596022	BLASTN	1266	1e-96	99
669	895	700021931H1	SATMON001	g596022	BLASTN	1126	1e-84	99
670	895	700805540H1	SATMON036	g596022	BLASTN	776	1e-55	99
671	895	700172576H1	SATMON013	g596022	BLASTN	571	1e-38	98
672	895	700105116H1	SATMON010	g596022	BLASTN	558	1e-37	99
673	895	700472931H1	SATMON025	g596022	BLASTN	379	1e-31	97
674	20643	LIB3069-009-Q1-K1-B3	LIB3069	g1100771	BLASTX	215	1e-44	50
675	2351	LIB3079-007-Q1-K1-C11	LIB3079	g1100771	BLASTX	304	1e-77	72
676	32930	LIB189-001-Q1-E1-E4	LIB189	g596022	BLASTN	794	1e-115	95
677	4222	LIB3079-001-Q1-K1-H7	LIB3079	g596022	BLASTN	1132	1e-101	89
678	895	LIB148-049-Q1-E1-D6	LIB148	g596022	BLASTN	2194	1e-178	97
679	895	LIB3066-052-Q1-K1-G8	LIB3066	g596022	BLASTN	2178	1e-172	97
680	895	LIB148-016-Q1-E1-G5	LIB148	g596022	BLASTN	1567	1e-161	99
681	895	LIB143-032-Q1-E1-E10	LIB143	g596022	BLASTN	1914	1e-155	99
682	895	LIB3061-013-Q1-K1-F7	LIB3061	g596022	BLASTN	1738	1e-136	88
683	895	LIB143-047-Q1-E1-D4	LIB143	g596022	BLASTN	1490	1e-119	88

SOYBEAN PHOSPHOGLUCOISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
684	-700568558	700568558H1	SOYMON002	g1369950	BLASTX	165	1e-15	80
685	-700845275	700845275H1	SOYMON021	g1100771	BLASTX	124	1e-10	53
686	-700960755	700960755H1	SOYMON022	g1100771	BLASTX	153	1e-14	52
687	18663	700838363H1	SOYMON020	g1100771	BLASTX	215	1e-22	63
688	18663	700838355H1	SOYMON020	g1100771	BLASTX	155	1e-14	81
689	19355	700897450H1	SOYMON027	g1100771	BLASTX	273	1e-31	74
690	19355	700744258H1	SOYMON013	g1100771	BLASTX	207	1e-29	69
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***Table Headings**

Cluster ID

A cluster ID is arbitrarily assigned to all of those clones which belong to the same cluster at a given stringency and a particular clone will belong to only one cluster at a given stringency. If a cluster contains only a single clone (a "singleton"), then the cluster ID number will be negative, with an absolute value equal to the clone ID number of its single member. The cluster ID entries in the table refer to the cluster with which the particular clone in each row is associated.

Clone ID

The clone ID number refers to the particular clone in the PhytoSeq database. Each clone ID entry in the table refers to the clone whose sequence is used for (1) the sequence comparison whose scores are presented and/or (2) assignment to the particular cluster which is presented. Note that a clone may be included in this table even if its sequence comparison scores fail to meet the minimum standards for similarity. In such a case, the clone is included due solely to its association with a particular cluster for which sequences of one or more other member clones possess the required level of similarity.

Library

The library ID refers to the particular cDNA library from which a given clone is obtained. Each cDNA library is associated with the particular tissue(s), line(s) and developmental stage(s) from which it is isolated.

NCBI gi

Each sequence in the GenBank public database is arbitrarily assigned a unique NCBI gi (National Center for Biotechnology Information GenBank Identifier) number. In this table, the

NCBI gi number which is associated (in the same row) with a given clone refers to the particular GenBank sequence which is used in the sequence comparison. This entry is omitted when a clone is included solely due to its association with a particular cluster.

Method

The entry in the "Method" column of the table refers to the type of BLAST search that is used for the sequence comparison. "CLUSTER" is entered when the sequence comparison scores for a given clone fail to meet the minimum values required for significant similarity. In such cases, the clone is listed in the table solely as a result of its association with a given cluster for which sequences of one or more other member clones possess the required level of similarity.

Score

Each entry in the "Score" column of the table refers to the BLAST score that is generated by sequence comparison of the designated clone with the designated GenBank sequence using the designated BLAST method. This entry is omitted when a clone is included solely due to its association with a particular cluster. If the program used to determine the hit is HMMSW then the score refers to HMMSW score.

P-Value

The entries in the P-Value column refer to the probability that such matches occur by chance.

%Ident

The entries in the "%Ident" column of the table refer to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented. This entry is omitted when a clone is included solely due to its association with a particular cluster.

We claim:

1. A substantially purified nucleic acid molecule that encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein said maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of:

(a) glucose-6-phosphate-1-dehydrogenase or fragment thereof;

(b) 6-phosphogluconate dehydrogenase or fragment thereof;

(c) putative 6-phosphogluconate dehydrogenase or fragment thereof;

(d) D-ribulose-5-phosphate-3-epimerase or fragment thereof;

(e) ribose-5-phosphate isomerase or fragment thereof;

(f) putative ribose-5-phosphate isomerase or fragment thereof;

(g) transketolase or fragment thereof;

(h) putative transketolase or fragment thereof;

(i) transaldolase or fragment thereof;

(j) putative transaldolase or fragment thereof;

(k) phosphoglucoisomerase or fragment thereof;

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699.

3. A substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein said maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of:

(a) glucose-6-phosphate-1-dehydrogenase or fragment thereof;

(b) 6-phosphogluconate dehydrogenase or fragment thereof;

(c) putative 6-phosphogluconate dehydrogenase or fragment thereof;

(d) D-ribulose-5-phosphate-3-epimerase or fragment thereof;

(e) ribose-5-phosphate isomerase or fragment thereof;

(f) putative ribose-5-phosphate isomerase or fragment thereof;

(g) transketolase or fragment thereof;

(h) putative transketolase or fragment thereof;

(i) transaldolase or fragment thereof;

(j) putative transaldolase or fragment thereof;

(k) phosphoglucoisomerase or fragment thereof;

4. A substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof according to claim 3, wherein said maize or soybean phosphogluconate pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean phosphogluconate pathway enzyme or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

(c) a nucleic acid sequence which encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

(d) a nucleic acid sequence which encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof;

(f) a nucleic acid sequence which encodes for an putative ribose-5-phosphate isomerase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for a transketolase enzyme or fragment thereof;

(h) a nucleic acid sequence which encodes for a putative transketolase enzyme or fragment thereof;

(i) a nucleic acid sequence which encodes for a transaldolase enzyme or fragment thereof;

(k) a nucleic acid sequence which encodes for a putative transaldolase enzyme or fragment thereof;

(l) a nucleic acid sequence which encodes for a phosphoglucoisomerase enzyme or fragment thereof;

(m) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (l); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (l).

8. A method for determining a level or pattern in a plant cell of a phosphogluconate pathway enzyme in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said phosphogluconate pathway enzyme;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said phosphogluconate pathway enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.

ABSTRACT

The present invention is in the field of plant biochemistry. More specifically the invention relates to nucleic acid sequences from plant cells, in particular, nucleic acid sequences from maize and soybean associated with the phosphogluconate pathway enzymes. The invention encompasses nucleic acid molecules that encode proteins and fragments of proteins. In addition, the invention also encompasses proteins and fragments of proteins so encoded and antibodies capable of binding these proteins or fragments. The invention also relates to methods of using the nucleic acid molecules, proteins and fragments of proteins and antibodies, for example for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants.

<110> Cheikh, Nordine
Liu, Jingdong
Peschke, Virginia M.

<120> Nucleic Acid Molecules And Other Molecules Associated With The Phosphogluconate Pathway

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tgcttgaaaa gggcttccca attccggtta acaacggaac catttccaag gttattgggc 180

cataagacga agcaaaccag gaaggaaacc ttcaatttat ggggaacaa 229

<210> 28
<211> 250
<212> DNA
<213> Glycine max

<400> 28

aatgaatctg atcagggcaa agagcattga gaaaggttgg gacttgaagt tgggggaact 60

tgcaaggatt tggaaagggg gttgcatcat aagagcaata tttttggaca gaatcaagaa 120

agcatacgac agaaatccta accttgcaaa ccttcttgtg gatccagaat ttgcaaagga 180

aatagtggat agacaatctg catggagaag agttgtgtgt cttgctatca actatggcac 240

tagcacacca 250

<210> 29
<211> 87
<212> DNA
<213> Glycine max

<400> 29

ggctcgaggg ggtcttacca cactgagtgg ttcaagcttg ccaaacagtc aagaaattag 60

agtactgtag tgcagccaat caggatc 87

<210> 30
<211> 256
<212> DNA
<213> Glycine max

<400> 30

attcttctca aggtggcagc tcaagtccct gacagtggtc cttgcgtgac ttatattggt 60

aaaggtggct ctggtaattt tgtgaaaatg atccacaatg gcatcgaata tggtgacatg 120

cagctgattg cagaggccta tgatgtgctg aagtcagttg gaaagttgtc aaatgaggaa 180

ctacaaagtg tcttctcaga atggaacaag ggagaacttc tgagtttcct gattgaaatc 240

actgcagata tatttg 256

<210> 31
<211> 213
<212> DNA
<213> Glycine max

<400> 31

gcgtgactta tattggtaaa ggtggctctg gtaattttgt gacaatgatc cacaatggca 60

tcgaatctgg tgacatgcag ctgattgcag aggcctatga tgtgctgaag tcagttggaa 120

agttgtcaaa tgaggaacta caaagtgtct tctcagaatg gaacaaggga gaacttctcg 180

agtttcctga ttgacatcac tgcagatata ttt 213

<210> 32

<211> 268
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 32

gtggcagctc aagtccctga cagtggtcct tgcgtgactt atattggtaa aggtggctct 60

ggtaattttg tgaaaatgat ccacaatggc atcgaatatg gtgacatgca gctgattgca 120

gaggcctatg atgtgctgaa gtcagttgga aagttgtcaa atgaggaact acaaagtgtc 180

tcctcagaat ggaacaaggg agaattctga gtttccgatt ganatcatgc agatatattg 240

gattcangag ataagggaga nggatacc 268

<210> 33
<211> 109
<212> DNA
<213> Glycine max

<400> 33

aaattttgtg aaaatgatcc acaatggaat tgagtatggt gacatgcagc tcattgctga 60

ggcctatgat gtgctaaagt cggttggaaa gttgtcaaat gaggagctg 109

<210> 34
<211> 277
<212> DNA
<213> Glycine max

<400> 34

gggcactggt aagtggactg ttcagcaagg tgctgaatta tcaattgctg ctcccactat 60

tgaagcatca ttggatgcaa ggttcctgag tgggttgaag gaggaaagag ttgaagctgc 120

aaaggtcttt aaatcaggtg gtattggtga tatcgtgact gatcaacctg tagacaagaa 180

aaaattggtt gatgatgtta ggaaggctct ttatgcagcc aaaatctgta gttatgcaca 240

gggaatgaat ttgatccgtg caaagagtat tgaaaag 277

<210> 35
<211> 252
<212> DNA
<213> Glycine max

<400> 35

gcaaggttcc tgagtgggtt gaaggaggaa agagttgaag ctgcaaaggt ctttaaatca 60

ggtggcattg gtgatattgt gactgatcaa cctgtagaca agcagaagtt gattgatgat 120

gttaggaagg ctctttatgc agccagaatc tgtagttatg cacagggaat gaatttgatc 180

cgtgcaaaga gtattgaaaa gggttgggat ttgaagttgg gtgaactggc ccggatttgg 240

aaaggggtt gc 252

<210> 36
<211> 262
<212> DNA
<213> Glycine max

<400> 36

cttgttgaca aggtcctaga caagactggc atgaagggca ctggtcaagt ggactgggca 60

gcaagctgct gaattatcaa ttgctgctcc cactattgaa gcatcattgg atgcaaggtt 120

cctgagtggg ttgaaggagg aaagacttga agctgcaaag gtctttaaat caggtggtat 180

tgctgatatc gtgactgatc aacctgtaga caagaaaaaa ttggttgatg atgttaggaa 240

ggctctttat gcagccaaaa tc 262

<210> 37
<211> 241
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 37

tttggaatta aggatgataa gggagatgga tatcttgttg acaaggtcct agacaagact 60

ggcatgaagg gcactggtaa gtggactgtt cagcaagctg ctgaattatc aattgctgct 120

cccactattg angcatcatt ggatgcaagg ttcctgagtg ggttgaagga ggaagagttg 180

aagctgcaaa ggtctttaaa tcaggtggta ttggtgatat cgtgactgat caacctgtag 240

a 241

<210> 38
<211> 239
<212> DNA
<213> Glycine max

<400> 38

aaagtgtctt ctcagaatgg aacaagggag aacttctgag tttcctgatt gaaatcactg 60

cagatatatt tggaattaag gatgataagg gagatggata tcttgttgac aagcgtccta 120

gacaagactg gcatgaaggg cactggtaag tggactgttc agcaagctgc tgaattatca 180

attgctgctc ccactattga agcatcattg gatgcaaggg tcctgagtgg ggtgaagga 239

<210> 39
<211> 252
<212> DNA
<213> Glycine max

<400> 39

ggagatggat tcttgttgac aaggtcctag acaagactgg catgaagggc actggtaagt 60

ggactgttca gcaagctgct gaattatcaa ttgctgctcc cactattgaa gcatcattgg 120

atgcaaggtt cctgagtggg ttgaaggagg aaagagttga agctgcaaag gtctttaaat 180

caggtggtat tggtgatatc gtgactgatc aacctgtaga caagaaaaaa ttggttgata 240

tgttaggaag gc 252

<210> 40
<211> 262
<212> DNA
<213> Glycine max

<400> 40

ctcgagccgt tcttagacag aatcaagcag gcatatgaaa gaacccctaa tctggcaaac 60

cttcttgtgg atccagagtt tgcaaaggaa ataattgatt accaatctgc ctggaggaga 120

gttgtttgcc ttgctatcaa ttctggtatt agcactccag gtatgtctgc tagtcttgct 180

tattttgaca cttacagaag ggaaaggttg ccagctaatt tggtgcaagc tcaacgagac 240

tactttggtg ctcatacata tg 262

<210> 41
<211> 167
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 41

acccttcttgt ggatccagag tttgcaangg aaataatcga tcgccaatct gcctggagga 60

gagttgtttg ccttgctatc aattctggta tcagcactcc aggtatgtct gctagtctng 120

cttatnttga cacttacaga agggaaaggt nnccagctaa tttggtg 167

<210> 42
<211> 230
<212> DNA
<213> Glycine max

<400> 42

gtgatagcga tgtccgaatt gggtcttctc taccttggga tgggagtttc aggtggtgaa 60

gaaggtgcaa gacatggtcc ctctttgatg cctggtggtt cattcgagga ctacaagtac 120

atagaagaca ttctcctcaa ggtagacgca caagtccctg atagtggtca ttgtgtgacc 180

tacatcggca aaggtggatc aggaaatttt gtgaaaatga tccacaatgg 230

<210> 43
<211> 245
<212> DNA
<213> Glycine max

<400> 43

gtgaaagcga tgtccgaatt gggtcttctc taccttggga tgggagtttc aggaggtgaa 60

gaaggtgcaa gacatggtcc ctctttgatg cctggtggtt cattcgaggc ctacaagtac 120

atagaagaca ttctcctcaa ggtggccgca caagtccctg atagtggtcc ttgtgtgacc 180

tacatcggca aaggtggatc aggaaatttt gtgaaaatga tccacaatgg aattgagtat 240

ggtga 245

<210> 44
<211> 289
<212> DNA
<213> Glycine max

<400> 44

atctgcctgg aggagagttg tttgccttgc tatcaattct ggtattagca ctccaggtat 60

gtctgctagt cttgcttatt ttgacactta cagaagggaa aggttgccag ctaatttggt 120

gcaagctcaa cgagactact ttggtgctca tacatatgaa agggttgaca tagaggggtc 180

ttaccatact gagtggttca agcttgccaa acagtcaaga aattagatta ctgtatttga 240

gccatcagga ttttcctaat aaatgtaata ttgtctgctc agactgtat 289

<210> 45
<211> 272
<212> DNA
<213> Glycine max

<400> 45

tcaggtatgt ctgctagtct tgcttatttt gacacttaca gaagggaaag gttgccagct 60

aatttggtgc aagctcaacg agactacttt ggtgctcata catatgaaag ggttgacata 120

gaggggtctt accatactga gtggttcaag cttgccaaac agtcaagaaa ttagattact 180

gtatttgagc caatcaggat tttcctaata aatgtaatat tttctgctca gactgtatgc 240

tgagttgagt ttgcatatcc acaatgtggt ga 272

<210> 46
<211> 246
<212> DNA
<213> Glycine max

<400> 46

ctaagataca acatagttgg aaaacaaact atcaagcaat tcagttggaa ataatataaa 60

taaaacttca ccacgttgtg gctatgtaaa ctcaactcag catacagtct gagcagaaaa 120

cattacattt attaggaaaa tcctgattgg ttcaaataca gtaatctaaa ttctagactg 180

tttggcaagc ttgaaccact cagtatggta agacccctct atgtcaacca ttcatatgta 240

tgagca 246

<210> 47
<211> 156
<212> DNA
<213> Glycine max

<400> 47

ggggtcttac catactgagt ggttcaagct tgccaaacag tcaagaaatt agattactgt 60

atttgagcca atcaggattt tcctaataaa tgtaatattt tctgctcaga ctgtatgctg 120

agttgagttt gccaagcaat tcagttggaa ataatg 156

<210> 48
<211> 250
<212> DNA
<213> Glycine max

<400> 48

tatggctacc atgaccccga agcttttgtt cattccattc aaaagcctag ggtgataata 60

atgcttgtta aggctggggc acctgttgac cagaccatta agaccctatc tgcatacatg 120

gaaaaaggtg actgcataat tgatggtggt aacgaatggt acgagaacac cgaaaggaga 180

gagaaatcgg tggctgaatt gggtctgctc taccttggga tgggagtttc tggtggtgag 240

gaaagtgctc 250

<210> 49
<211> 170
<212> DNA
<213> Glycine max

<400> 49

ggcacctgtt gaccagacca ttaagaccct atctgcatac atggaaaaag gtgactgcat 60

aattgatggt ggtaacgaat ggtacgagaa caccgaaaga agagagaaat cggtggctga 120

attgggtctg ctctaccttg ggatgggagt ttctggtggt gaggaaggtg 170

<210> 50
<211> 275
<212> DNA
<213> Glycine max

<400> 50

gacgacagaa gggagaaatc ggtggctgaa ttgggtctgc tctacctcgg gatgggagtt 60

tctggtggtg aggaaggtgc tcgtaatggt ccctctttga tgcctggtgg ttcgtttgag 120

gctttcaaat acatagaaga tattcttctc aaggtggcag ctcaagtccc tgacagtggt 180

ccttgcgtga cttatattgg taaaggtggc tctggtaatt ttgtgaaaat gatccacaat 240

ggcatcgaat atggtgacat gcagctgatt gcaga 275

<210> 51
<211> 256

<212> DNA
<213> Glycine max

<400> 51

acggctgcga gaagacgaca gaagggggaa aaaggtgact gtataattga tggtggtaac 60

gaatggtatg agaacactga aagaagagag aaagaggtgg ctgaattggg tctgctctac 120

cttgggatgg gagtttctgg tggtgaggaa ggtgctcgta atggtccctc tttgatgcct 180

ggtggttcgt ttgaggcttt caaatacata gaagatattc ttctcaaggt ggcagctcaa 240

gtacctgaca gtggtc 256

<210> 52
<211> 252
<212> DNA
<213> Glycine max

<400> 52

gactgccata ttgatggtgg taacgaatgg tacgagaaca ccgaaagaag agagaaatcg 60

gtggctgaat tgggtctgct ctaccttggg atgggagttt ctggtggtga ggaaggtgct 120

cgtaatggtc ctctttgatg cctggtggtt cgtttgaggc tttcaaatac atagaagata 180

ttcttctcaa ggtggcagct caagtccctg acagtggtcc ttgcgtgact tatattggta 240

aaggtggctc tg 252

<210> 53
<211> 346
<212> DNA
<213> Glycine max

<400> 53

gtgaagttaa ggaaatcaat tatggctcaa ccctcaacaa gaatagggcc ttgctggact 60

ggctgttatg ggccaaaatc tagcactcaa tattgctgag aaaggctttc ccatttctgt 120

ttataaccga accacttcca aggttgatga gactgtagaa cgagcaaaac aagaaggaaa 180

tcttccagtt tatggctacc atgaccccga agcttttgtt cattccattc aaaagcctag 240

ggtgataata atgcttgtta aggctggggc atctgttgac cagaccatta agaccctatc 300

tgcatacatg gaaaaaggtg actgcataat tgatggtggt aacgaa 346

<210> 54
<211> 283
<212> DNA
<213> Glycine max

<400> 54

ccagacctta atttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat 120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc 240

ttttgtcatt ccattcaaaa gcctagggtg ataataatgc ttg 283

<210> 55
<211> 276
<212> DNA
<213> Glycine max

<400> 55

caaatttcag gaaatcaatt atggctcaac cctcaacaag aataggcctt gctggactgg 60

ctgttatggg ccaaaatcta gcactcaata ttgctgagaa aggctttccc atttctgttt 120

ataaccgaac cacttccaag gttgatgaga ctgtagaacg agcaaaacag gaaggaaatc 180

ttccagttta tggctaccat gaccccgaag cttttgttca ttccattcaa aagcctaggg 240

tgataataat gcttgttaag gctggggcac ctgttg 276

<210> 56
<211> 289
<212> DNA
<213> Glycine max

<400> 56

cagaccttaa ttgttctctc attcgcttca aatttcagga aatcaattat ggctcaaccc 60

tcaacaagaa taggccttgc tggactggct gttatgggcc aaaatctagc actcaatatt 120

gctgagaaag gctttcccat ttctgtttat aaccgaacca cttccaaggt tgatgagact 180

gtagaacgag caaaacaaga aggaaatctt ccagtttatg gctaccatga ccccgaagct 240

tttgttcatt ccattcaaaa gcctagggtg ataataatgc ttgttaagg 289

<210> 57
<211> 267
<212> DNA
<213> Glycine max

<400> 57

cctcattcgc ttcaaatttc aggaaatcaa ttatggctca accctcaaca agaataggcc 60

ttgctggact ggctgttatg ggccaaaatc tagcactcaa tattgctgag aaaggctttc 120

ccatttctgt tttaaccgaa ccacttccaa ggttgatgag actgtagaac gagcaaaaca 180

agaaggaaat cttccagttt atggctacca tgaccccgaa gcttttgttc attccattca 240

aaagcctagg gtgataataa tgcttgt 267

<210> 58
<211> 260
<212> DNA
<213> Glycine max

<400> 58

ccagacctta atttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat 120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc 240

ttttgttcat tccattcaaa 260

<210> 59
<211> 260
<212> DNA
<213> Glycine max

<400> 59

tgtgattcca gaccttaatt tttctctcat tcgcttcaaa tttcaggaaa tcaattatgg 60

ctcaaccctc aacaagaata ggccttgctg gactggctgt tatgggccaa aatctagcac 120

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg 180

atgagactgt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc 240

ccgaagcttt tgttcattcc 260

<210> 60
<211> 265
<212> DNA
<213> Glycine max

<400> 60

cagaccttaa tttttctctc attcgcttca aatttcaggg gatcaattat ggctcaaccc 60

tcaacaagaa tatgccttgc tggactggct gttatgggcc agaatctagc actcaatatt 120

gctgagaaag gctttcgcat ttctgtttat aaccgaacca cttccaaggt tgatgagact 180

gtagaacgag caaaacaaga aggaaatctt ccagtttatg gctaccatga ccccgaagct 240

tttgttcatt ccattcaaaa gccta 265

<210> 61
<211> 263
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 61

ctagacctta atttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggt ccaaatctag cactcaatat 120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgtagaacta gcannacaag aaggaaatct tccagtttat ggctaccatg accccgaagc 240

ttttgttcat tccattcaaa agc 263

<210> 62
<211> 279
<212> DNA
<213> Glycine max

<400> 62

tgctctgtga ttccagacct taatttttcc ctcattcgct tcaaatttca ggaaatcaat 60

tatggctcaa ccctcaacaa gaataggcct tgcacctctg gctgttatgg gccaaaatct 120

agcactcaat attgctgaga aaggctttcc catttctgtt tataaccgaa ccacttccaa 180

ggttgatgag actgtagaac gagcaaaaca agaaggaaat cttccagttt atggctacca 240

tgaccccgaa gcttttgttc attccattca aacgcctag 279

<210> 63
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 63

tgattccaga ccttaatttt tctctcattc gcttcaaatt tcaggaaatc aattatggct 60

caaccctcaa caagaatagg ccttgctgga ctggctgtta tgggccaaaa tctagcactc 120

natattgctg agaaaggctt tcccatttct gnttataacc gnaccacttc caaggntgat 180

gagactgtag nacgagcnaa acaggaagga aatcttccag tttatggcta ccatgacccc 240

gnagctttgt tcattccatt caaaagctag ggtgataata atgc 284

<210> 64
<211> 256
<212> DNA
<213> Glycine max

<400> 64

gtgattccag accttaattt ttctctcatt cgcttcaaat ttcaggaaat caattatggc 60

tcaaccctca acaagaatag gccttgctgg actggctgtt atgggccaaa atctagcact 120

caatattgct gagaaaggct ttcccatttc tgtttataac cgaaccactt ccaaggttga 180

tgagactgta gaacgagcaa aacaggaagg aaatcttcca gtttatggct accatgaccc 240

cgaagctttt gttcat 256

<210> 65
<211> 265
<212> DNA
<213> Glycine max

<400> 65

ccgtgctctg tgattccaga ccttaatttt tctctcattc ccttcaaatt tcaggaaatc 60

aattatggct caaccctcaa caagaatagg ccttgctgga ctggctgtta tgggccaaaa 120

tctagcactc aatattgctg agaaaggctt tcccatttct gtttataacc gaaccacttc 180

caaggttgat gagactgtag aacgagcaaa acaagaagga aatcttccag tttatggcta 240

ccatgacccc gaagcttttg ttcat 265

<210> 66
<211> 275
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 66

gtgattccca gaccttattt nttctgtcat ttgcttcaaa tttcaggaga ttaattatgg 60

ctcaacccan aacaagaata ggccttnctg gattggctgt tatgggccaa aatctggcac 120

tcaatattgc tgagaaaggc ttncccattt ctgtttacaa ccgaaccact tccaaggttg 180

atgagacagt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc 240

ctgaagcttt tgttcattcc attcaanagc ctagg 275

<210> 67
<211> 236
<212> DNA
<213> Glycine max

<400> 67

cagaccttaa tttttctctc attcgcttca aatttcagga aatcaattat ggctcaaccc 60

tcaacaagaa taggccttgc tggactggct gttatgggcc aaaatctagc actcaatatt 120

gctgagaaag gctttcccat ttctgtttat aaccgaacca cttccaaggt tgatgagact 180

gtagaacgag caaaacagga aggaaatctt ccagtttatg gctaccatga ccccga 236

<210> 68
<211> 280
<212> DNA
<213> Glycine max

<400> 68

cacagacctt atgatttctg tcatttacat caaatttcag gagattaatt atggctcaac 60

ccataacaag aataggcctt gctggattgg ctgttatggg ccaaaatctg gcactcaata 120

ttgctgagaa aggctttccc attctgttta caaccgaacc acttccaagg ttgatgagac 180

agtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accctgaagc 240

ttttgttcat tccattcaaa agcctagggt gatactaatg 280

<210> 69
<211> 281
<212> DNA
<213> Glycine max

<400> 69

ctgtgattcc cagaccttat tttttctgtc atttgcttca agtctcagga gattgattat 60

ggctcaaccc acaacaagaa taggccttgc tggattggct gttatgggcc aaaatctggc 120

actcaatatt gctgagaaag gctttcccat ttctgtttac aaccgaacca cttccaaggt 180

tgatgagaca gtagaacgag caaaacaaga aggaaatctt ccagtttatg gctaccatga 240

ccctgaagct tttgttcatt ccattcaaaa gcctagggtg a 281

<210> 70
<211> 261
<212> DNA
<213> Glycine max

<400> 70

gattcccaga ccttattttt tctgtcattt gcttcaaatt tcaggagatt aattatggct 60

caacccacaa caagaatagg ccttgctgga ttggctgtta tgggccaaaa tctggcactc 120

aatattgctg agaaaggctt tcccatttct gtttacaacc gaaccacttc caaggttgat 180

gagacagtag aacgagcaaa acaagaagga aatcttccag tttatggcta ccatgaccct 240

gaagcttttg ttcattccat t 261

<210> 71
<211> 225
<212> DNA
<213> Glycine max

<400> 71

cttaatttgt ctctcattcg cttcaaattt caggaaatca attatggctc gaccctcgac 60

aagaataggc cttgctggac tggctgttat ggggcaaaat ctagcactca atattgctga 120

gaaaggcttt cccatttctg tttataaccg aaccacttcc aaggttgatg agactgtaga 180

acgagcaaaa caagaaggaa atcttccagt ttatggctac catga 225

<210> 72

<211> 265
<212> DNA
<213> Glycine max

<400> 72

ccagacctta atttttctct cattcgcttc agctttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat 120

tactgagaaa ggctgtccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgcagaacga gcaaaacaag aaggacatct tccagtttat ggctaccatg accccgaagc 240

ttttgttcat tccattcaaa agccc 265

<210> 73
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 73

cccgcatctt ttgatccgtg ctctgtgatt cccagacctt atttntnctg tcatttgctt 60

caaatntcag gagattaatt atggctcaac ccacaacaag aataggcctt gctggattgg 120

gctgttatgg gccaaaatct ggcactcaat attgctgaga aaggctttcc catttctgtt 180

tacanccgaa ccacttccaa ggttgatgag acagtagaac gagcaaanca aganggaaat 240

cttccagttt atggctacca tgaccctgaa gcttttgttc nttccatt 288

<210> 74
<211> 259
<212> DNA
<213> Glycine max

<400> 74

gatccgtgct ctgtgattcc cagaccttat tttttctctc atttgcttca aatttcagga 60

gattaattat ggctcaaccc acaacaagaa taggccttgc tggattggct gttatgggcc 120

aaaatctggc actcaatatt gctgagaaag gctttcccat ttctgtttac aaccgaacca 180

cttccaaggt tgatgagaca gtagaacgag caaaacaaga aggaaatctt ccagtttatg 240

gctaccatga ccctgaagc 259

<210> 75
<211> 250
<212> DNA
<213> Glycine max

<400> 75

tccagacctt aatttttctc tcattcgctt caaatttcag gaaatcaatt atggctcaac 60

cctcaacaag aataggcctt gctggactgg ctgttatggg ccaatatcta gcactcaata 120

ttgctgagaa aggtttccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc 240

ttttgttcat 250

<210> 76
<211> 220
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 76

cnagacctta atttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat 120

tgctgagaaa ggctttccca tttcgncnta taaccgaacc acttccaagg ttgatgagac 180

tgtagaacga gcaaaacaag aaggaaatct tccagtttnt 220

<210> 77
<211> 230
<212> DNA
<213> Glycine max

<400> 77

tgtgattcca gaccttaatt tttctctcat tcgcttcaaa tgtcaggaaa tcaagtatgg 60

ctcaaccctc cacaagagta ggccttgctg gactggctgt tatgggccca aatctagcac 120

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg 180

atgagactgt agaacgagca aaacctgaag gcaatcttcc agtttatggc 230

<210> 78
<211> 259
<212> DNA

<213> Glycine max

<400> 78

cttattttttt ctgtcatttg cttcaaattt caggagatta attatagctc aacccacaac 60

aagaataggc cttgctggat tggctgttat gggccaaaat ctggcactca atattgctga 120

gaaaggcttt cccatttctg tttacaaccg aaccacttcc aaggttgatg agacagtaga 180

acgagcaaaa caagaaggaa atcttccagt ttatggctac catgaccctg aagcttttgt 240

tcattccatt caaaagcct 259

<210> 79
<211> 256
<212> DNA
<213> Glycine max

<400> 79

cttttgatcc gtgctctgtg attcccagac cttatttttt ctgtcatttg cttcaaattt 60

caggagatta attatggctc aacccacaac aagaataggc cttgctggat tggctgttat 120

gggccaaaac tggcactcaa tattgctgag aaaggctttc ccatttctgt ttacaaccga 180

accacttcca aggttgatga gacagtagaa cgagcaaaac aagaaggaaa tcttccagtt 240

tatggctacc atgacc 256

<210> 80
<211> 253
<212> DNA
<213> Glycine max

<400> 80

cccagacctt attttttctg tcatttgctt caaatttcag gagataatta tggctcaacc 60

cacaacaaga ataggccttg ctggattggc tgttatgggc caaaatctgg cactcaatat 120

tgctgagaaa ggctttccca tttctgttta caaccgaacc acttccaagg ttgatgagac 180

agtagaacga gcataacaag aaggaaatct tccagtttat ggctaccatg accctgaagc 240

ttttgttcat tcc 253

<210> 81
<211> 198
<212> DNA

<213> Glycine max

<400> 81

ccagacctta atttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc 60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat 120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac 180

tgtagaccga gcaaaaca 198

<210> 82
<211> 281
<212> DNA
<213> Glycine max

<400> 82

atataatata catacatata tatataactt attccccgc atcttttgat ccgtgctctg 60

tgattcccag accttatttt ttctgtcatt tgcttcaaat ttcaggagat taattatggc 120

tcaacccaca acaagaatag gccttgctgg attggctgtt atgggccaaa atctggcact 180

caatattgct gagaaaggct ttcccatttc tgtttacaac cgaaccactt ccaaggttga 240

tgagacagta gaacgagcaa aacaagaagg aaatcttcca g 281

<210> 83
<211> 245
<212> DNA
<213> Glycine max

<400> 83

tcgatcgggt atcacatctg aattgggact gctcctattc tgggtactat tctgagaata 60

attatggctc aacccacaac aagaataggc cttgctggat tggctgttat gggccaaaat 120

ctggcactca atattgctga gaaaggcttt cccatttctg tttacaaccg aaccacttcc 180

aaggttgatg agacagtaga acgagcaaaa caagaaggaa atcttccagt ttatggctac 240

catga 245

<210> 84
<211> 230
<212> DNA
<213> Glycine max

<400> 84

aaccgaacca cttccaaggt tgtaaacaga aatgggaaag cctttctcag caatattgag 60

tgccagattt tggcccataa cagccaatcc agcaaggcct attcttgttg tgggttgagc 120

cataattaat ctcctgaaat ttgaagcaaa tgacagaaaa aataaggtct gggaatcaca 180

gagcacggat caaaagatgc gggggaataa gttatatata tatgtatgta 230

<210> 85
<211> 88
<212> DNA
<213> Glycine max

<400> 85

ggctcgagct cagtcgcttc aaatttcagg aaatcaatta tggctcaacc ctcaacaaga 60

ataggccttg ctggactggc tgttatgg 88

<210> 86
<211> 202
<212> DNA
<213> Glycine max

<400> 86

caaaaagcaa tctagctttg catactctac ctctacttca cctcgttacc aaaactagca 60

atcatgtctg tcgagcccaa gggagatgtc ggactcattg gtctggccgt tatgggtcaa 120

aacctgatcc tcaacatgaa cgacaagggt ttcaccgtcg tcgcctacaa ccgaaccacc 180

tccaaggtcg accacttcct gg 202

<210> 87
<211> 173
<212> DNA
<213> Glycine max

<400> 87

caaaaagcaa tctagctttg catactctac ctctacttca cctcgttacc aaaactagca 60

atcatgtctg tcgagcccaa gggagatgtc ggactcattg gtctggccgt tatgggtcaa 120

aacctgatcc tcaacatgaa cgacaagggt ttcaccgtcg tcgcctacaa ccg 173

<210> 88

<211> 237
<212> DNA
<213> Glycine max

<400> 88

aggaaacgcc tttcctgaga agtcggaagg aagagagtga gagtgagagt gagagtgaga 60

gagatggagt ttggattttt gggtttgggg ataatgggta aggctatggc aatcaatctg 120

ctacgccatg gcttcaaggt cactatttgg aacagaaccc tctccaagtg tgatgaactc 180

gtgcaacatg gtgcttcagt tggagaaacc ccagcaactg tagtcaagaa atgcaag 237

<210> 89
<211> 255
<212> DNA
<213> Glycine max

<400> 89

gattggtggt acactggaaa ttaaccatgg ctcaacctgc aagcctcaca agaataggcc 60

ttgctggcct ggctgtgatg ggccaaaacc ttgctctcaa cattgctgag aaaggctttc 120

ccatttctgt ctacaaccgg accgcgtcca aggttgatga gacagttgaa agagcaaaac 180

aagaaggaaa ccttcctgtg tatggctacc atgaccctaa attctttgtc caatccattc 240

aaaagccaag ggtca 255

<210> 90
<211> 256
<212> DNA
<213> Glycine max

<400> 90

ctttctcgca tgaattttcg aacattgaac aggaaattaa ccatggctca acctgcaagc 60

ctcacaagaa taggccttgc tggcctggct gtgatgggcc aaaaccttgc tctcaacatt 120

gctgagaaag gctttcccat ttctgtctac aaccggaccg cgtccaaggt tgatgagaca 180

gttgaaagag caaaacaaga aggaaacctt cctgtgtatg gctaccatga ccctaaattc 240

tttgtccaat ccattc 256

<210> 91
<211> 256
<212> DNA

<213>	Glycine max

<400>	91

cacccagatc tcaattttct gcaatttcac tcagaccagg aaattaacca tggctcaacc	60

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct	120

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga	180

tgagacagtt gaaagagcaa aacaagaagg aaaccttcct gtgtatggct accataaccc	240

taaattcttt gtccaa	256

<210>	92
<211>	249
<212>	DNA
<213>	Glycine max

<400>	92

cgatgccaca acttctgtgt tggattggtg gtacactgga aattaaccat ggctcaaaca	60

acaagcctca caagaatagg ccttgctggc ctggctgtga tgggccaaaa ccttgctctc	120

aacattgctg agaaaggctt tcccatttct gtctacaacc ggaccgcgtc caaggttgat	180

gagacagttg aaagagcaaa acaagaagga aaccttcctg tgtatggcta ccatgaccct	240

aaattcttt	249

<210>	93
<211>	250
<212>	DNA
<213>	Glycine max

<400>	93

ccagatctca attttctgca atttcactca gaccaggacc ttaaccatgg ctcaacctgc	60

aagcctcaca agaataggcc ttgctggcct ggctgtgatg ggccaaaacc ttgctctcaa	120

cattgctgac aaaggctttc ccatttctgt ctacaaccgg accgcgtcca aggttgatga	180

gacagttgaa agagcaaaac aagaaggaaa ccttcctgtg tatggctacc ataacctcaa	240

attctttgtc	250

<210>	94
<211>	273
<212>	DNA

<213>   Glycine max

<400>   94

gttaatttgc accttttgtt tctctctaga aattagaagt tcatgcttaa actttacctt   60

gatacttctt tctcgcatga attttcgaac attgaacagg aaattaacca tggctcaacc   120

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct   180

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga   240

tgagacagtt gaaagagcaa aacaagaagg aaa   273

<210>   95
<211>   250
<212>   DNA
<213>   Glycine max

<400>   95

gttaatttgc accttttgtt tctctctaga aattagaagt tcatgcttaa actttacctt   60

gatacttctt tctcgcatga attttcgaac attgaacagg aaattaacca tggctcaacc   120

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct   180

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga   240

tgagacagtt   250

<210>   96
<211>   307
<212>   DNA
<213>   Glycine max

<400>   96

caacagtgca tgcttgcaat tcaacttagt ctacagtgtc cttgtatatt actcttttgt   60

ccttgctcac ttgatgcttt ctacaatctc tgggacaccc agatctcaat tttctgcaat   120

ttcactcaga ccaggaaatt aaccatggct caacctgcaa gcctcacaag aataggcctg   180

ctggcctggg ctgtgatggg ccaaaacctt gctctcaaca ttgctgagaa aggctttccc   240

atttcgtcta caaccggacc gcgtccaagg ttgatgagac agttgaaaga gcaaacaaga   300

aggaact   307

<210>   97

<211> 241
<212> DNA
<213> Glycine max

<400> 97

ctaaaaagca cttcttagtt ctccctctcc cactaaaaac catagtactc tagataataa 60

ttaacatcaa ccctcactcc ttcgcacacc aaacccttcc ttcctatctc tcactaatct 120

aatggaatcc gcagcactgt cgcgcatagg cctggcgggc ctggcggtga tgggccaaaa 180

cctagcccta gacatcgcag aaaaggggtt cccgatctcc gtgtacaacc gcacggcctc 240

t 241

<210> 98
<211> 401
<212> DNA
<213> Glycine max

<400> 98

gcgtccatac gactgcgaga agacgacaga aggggatgtt aagaaggctc tttatgcagc 60

caaaatctgt agttatgcac agggaatgaa tttgatccgt gcaaacagta ttgagcgggg 120

ttgggatttg aagttgggtg aactggcccg gatttggaaa gggggttgca ttattagagc 180

aatattctta gacagaatca agcaggcata tgaaagaaac cctaatctgg caaaccttct 240

tgtggatcca gagtttgcac aggaaatcat tgattaccaa tctgcctgca ggagagttgt 300

ttgccttgct atcaattctg gtattagcac tccaggtatg tctgctaatc ttgcttattt 360

tgacacttac agaaaggaac agtttccagc caatttggtg c 401

<210> 99
<211> 435
<212> DNA
<213> Glycine max

<400> 99

cccacgcgtc cgtacggctg cgagaagacg acagaaggga gaaaaaattg gttgatgatg 60

ttaggaaggc tctttatgca gccaaaatct gtagttatgc acagggaatg aatttgatcc 120

gtgcaaagag tattgaaaag ggttgggatt tgaagttggg tgaactggcc cggatttgga 180

aaggtggttg catcattaga gcaatattct tagacagaat caagcaagcg tatgatagaa 240

accctaatct ggcaaacctt cttgtggatc cagagtttgc aaaggaaata atcgatcgcc 300

aatctgcctg gaggagagtt gtttgccttg ctatcaattc tggtatcagc actccaggta 360

tgtctgctag tcttgcttat tttgacactt acagaaggga aaggttgcca gctaatttgg 420

tgcaagctca acgag 435

<210> 100
<211> 376
<212> DNA
<213> Glycine max

<400> 100

cacgcgtcca tacggctgcg agaagacgac agaaggggat gttaggaagg ctctttatgc 60

agccaaaatc tgtagttatg cacagggaat gaatttgatc cgtgcaaaga gtattgaaaa 120

gggttgggat ttgaagttgg gtgaactggc ccggatttgg aaaggggtt gcattattag 180

agcaatattc ttagacagaa tcaagcaggc atatgaaaga aaccctaatc tggcaaacct 240

tcttgtggat ccagagtttg caaaggaaat aattgattac caatctgcct ggaggagagt 300

tgtttgcctt gctatcaatt ctggtattag cactccaggt atgtctgcta gtcttgctta 360

gtttgacact tacaga 376

<210> 101
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 101

acgcgtccgc ccacgcgtcc gtacggctgc gagaagacga cagaaggggg atccgtgctc 60

tgtgattcca gaccttaatt tttctctcat tcgcttcaaa tttcnggaaa tcaattatgg 120

ctcaaccctc aacaagaata ggccttgctg gactggctgt tatgggccaa aatctagcac 180

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg 240

atgagactgt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc 300

ccgaagcttt tgttcattcc attcaaaaac ctaaggtgat 340

<210> 102
<211> 354

<212> DNA
<213> Glycine max

<400> 102

agtacggctg cgagaagacg acagaagggg ttgccagcta atttggtgca agctcaacga 60

gactactttg gtgctcatac atatgaaagg gttgacatag aggggtctta ccatactgag 120

tggttcaagc ttgccaaaca gtctagaatt tagattactg tatttgaacc aatcaggatt 180

ttcctaataa atgtaatgtt ttctgctcag actgtatgct gagttgagtt tacatagcca 240

caacgtggtg aagttttatg tatattattt ccaactgaat tgcatgatag tttgttttcc 300

aactatgttg tatctttgct gattatgctt tgtgcttgat acaaaattgt ccca 354

<210> 103
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 103

aggctgcgag aagacgacag aagggggtgc tctatgattc ccagacctta tttttctgt 60

catttgcttc aaatttcagg gagattaatt atggctcaac ccacaacaag aataggcctt 120

gctggattgg ctgttatggg ccaaaatctg gcactcaata ttgctgagaa aggctttccc 180

atttctgttt acaaccgaac cacttccaag gttgatgaga cagtagaacg agcaaaacaa 240

gaaggaaatc ttccagttta tggctaccat gaccctgaag cttttgttca ttccattcaa 300

aagcctaagg tgataataat gcttgttaag gctggggcac ctgttgacca gaccattaag 360

aacctatctg cgtacatgga anaaagtgac tgtataatt 399

<210> 104
<211> 179
<212> DNA
<213> Zea mays

<400> 104

gagctgtcgg tggccgctcc tacgatcgag gcgtccttgg actcgaggtt cctgagcggg 60

ctgaaggacg agcgggtgga tgcctccaag atcttccatg gtgactacta ctccaccggc 120

tcgccggtgg acaaggcgca ctggttggag gacgtgatgc aggccctgta cgcgtccaa 179

<210> 105
<211> 270
<212> DNA
<213> Zea mays

<400> 105

tagcgcgacg gccgcccttt tttttttttt ttgagaatca tcatagcaat tgcataccaa 60

aattaagaga atcaaactgt gcgtacctac atcacagtaa aactgaagct acacaatgtt 120

cttcacttgc caaccataca gtacagcatt atttgaagta ctcgacttgg atctagaagc 180

ataaagataa caatagtaaa acaaaagata acccacagag agacatcaca caaagcagac 240

aacatcactt ctcataccaa ccaattcctc 270

<210> 106
<211> 291
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 106

ccgcaacgnn cncgtccttg atgcccggan gctcgttcga cgcttacaag tacgtcgaag 60

acattgttct caaggtggct gctcaggtcc ctgacagtgg cccgtgtgtn acgtacattg 120

gcaaaggtgg atcgggcaac tttgtcaaga tggttcacaa cggaatcgag tatgggcgat 180

atgcagctga tttccgaggc ttacgacgtt ctcaagtcgg tcggtaagct caccaacagt 240

gagctgcacc aggtgttctc cgagtggaac aagggcgagt cctgagttct t 291

<210> 107
<211> 287
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 107

cgcagacgga ggacggcgcc tgcgtcacct tcgtcgggcc cggcggcgcc ggcaacttcg 60

tcaagatggt gcacaacggg ancgagtacg gcgacatgca gcaccatcgc cgaggcgtac 120

gacgtgctcc gcaggctcgg gggcctgtcc aactccgaga tcgccgatgt cttcgctgag 180

tggaacaggg gggagctcga gagcttcctg gtcnagatca ccgccgacat tttcaccgtg 240

gctgacccgt tggacgggag cgggagtggc ggcggggcgt ggttgat 287

<210> 108
<211> 192
<212> DNA
<213> Zea mays

<400> 108

cggcgacatg cagctcatcg ccgaagcgta cgacgtgctc cgcaggctcg ggggcctgtc 60

caactccgag atcgccgacg tcttcgcgga gtggaacagg ggggagctcg agagcttcct 120

ggtccagatc atcgccgaca ttttcatcgt gctgacccgt tagactggag ctggatcggc 180

ggtcaggacg ct 192

<210> 109
<211> 281
<212> DNA
<213> Zea mays

<400> 109

gatggctgct caggtacctg ttagcggccc gtgcgtcaca tgtattggca aatgtggatc 60

agggaacttc gtcaagatgc ttcacaattg aattgagtat ggttgcatgc aacttatcga 120

cgaggcttat gatttactca agtcggtgag taagctcatc aacagcgagc tgcatcaggt 180

attctctgag tgtgaatcaa ggtgagctcc tcagtatctt gattaagatc acggccgaca 240

tcgttggtat ctaggatcac aagggtgaat gctacctcgt c 281

<210> 110
<211> 325
<212> DNA
<213> Zea mays

<400> 110

tagcgctcac aagaatcggt cttgctgagc ctgcgtgtca tggcggcaga aacttgccct 60

caacattgca gaggaagggt tccccatctc tgtgtacaac aggagaagct ccaaggtgga 120

cgagaccgtg ccacgtgcca acgcagtacg aaaccttccc gtctagggct tccatgaccc 180

cgcgttcgtt gtgaagtcca ttcagaagcc acgggtggtg atcatgctcg tcaaagccgg 240

cgcgcagttg accagaccat cgcgactctc gcagctcact tggagcaggg cgactgcatc 300

atcgctcgtg ggaacgagtg gtacg 325

<210> 111
<211> 222
<212> DNA
<213> Zea mays

<400> 111

aaagggacag ggaagtggac ggtgcagcag gccgccgagc tgtcggtggc cgctcctacg 60

atcgaagcgt tcttggactc gaggttcctg agcgggctga aggacgagcg ggtggaggcc 120

tccaagatct tccagggtga ctactactcc accggctcgc cggtggacaa ggcgcagctg 180

gtggaggacg tgaggcaggc cctgtacgcg tacaagatct gc 222

<210> 112
<211> 334
<212> DNA
<213> Zea mays

<400> 112

tgactactcc actggcctac cggtggacaa ggcacagctg atcgaggacg tgaggcaagc 60

tctatatgcc tccaagatct gcagttacgc gcagggcatg aacatcatca aggccaagag 120

ctcagagaaa ggatggggcc tcaaccttgg tgagctagcg aggatctgga agggagggtg 180

catcatccgt gccatcttcc tcgaccgcat caagaaggcg tacgatagga accctaacct 240

tgccaacctc ctcgttgacc ccgagttcgc ccaggagatc atagacaggc aagctgcctg 300

gcgcagggtt gtctgccttg ccatcaacaa tggc 334

<210> 113
<211> 314
<212> DNA
<213> Zea mays

<400> 113

gaggcctcca agatcttcca gggtgactac tactccaccg gctcgccggt ggacaaggcg 60

cactgagtgg aggacgtgag gcaggccctg tacgcgtcca agatctgcag ctacgcgcag 120

ggcatgaaca tcatcaaggc caagagcgcg gagaaaggct ggggcgtcga cctcggcgaa 180

ctggcacagg atctagaagg gcgggtgcat catccgcgcc atcttcctgg accgcatcaa 240

gaaggcctac gacaggaacc cgggcctcgc cagcctgctc gtagaccccg agttcgcgca 300

ggagatcatg gaca 314

<210> 114
<211> 271
<212> DNA
<213> Zea mays

<400> 114

gaggcaagct ctatatgcct ccaagatctg cagttacgcg cagggcatga acatcatcaa 60

ggccaagagc tcagagaaag gatggggcct caaccttggt gagctagcga ggatctggaa 120

gggagggtgc atcatccgtg ccatcttcct cgaccgcatc aagaaggcgt acgataggaa 180

ccctaacctt gccaacctcc tcgttgaccc cgagttcgcc caggagatca tagacaggca 240

agctgcctgg cgcagggttg tctgccttgc c 271

<210> 115
<211> 271
<212> DNA
<213> Zea mays

<400> 115

ctccactggc ctaccggtgg acaaggcaca gctgatcgag gacgtgaggc aagctctata 60

tgcctccaag atctgcagtt acgcgcaggg catgaacatc atcaaggcca agagctcaga 120

gaaaggatgg ggcctcaacc ttggtgagct agcgaggatc tggaagggag ggtgcatcat 180

ccgtgccatc ttcctcgacc gcatcaagaa ggcgtacgat aggaacccta accttgccaa 240

cctcctcgtt gaccccgagt tcgcccagga g 271

<210> 116
<211> 289
<212> DNA
<213> Zea mays

<400> 116

gaggacgtga ggcaagctct atatgcctcc aagatctgca gttacgcgca gggcatgaac 60

atcatcaagg ccaagagctc agagaaagga tggggcctca accttggtga gctagcgagg 120

atctggaagg gagggtgcat catccgtgcc atcttcctcg accgcatcaa gaaggcgtac 180

gataggaacc ctaaccttgc caacctcctc gttgaccccg agttcgccca ggagatcata 240

gacaggcaag ctgcctggcg cagggttgtc tgccttgcca tcaacaatg 289

<210> 117
<211> 266
<212> DNA
<213> Zea mays

<400> 117

ctacgcgcag ggcatgaaca tcatcaaggc caagagcgcg gagaaaggct gggggctcaa 60

cctcggcgag ctggccagga tctggaaggg cgggtgcatc atccgcgcca tcttcctgga 120

ccgcatcaag aaggcctacg acaggaaccc gggcctcgcc agcctgctcg tagaccccga 180

gttcgcgcag gagatcatgg acaggcaggc ggcgtggcgc agggtggtgt gcctcgccat 240

caacaacggc gtcagacccc gggaat 266

<210> 118
<211> 264
<212> DNA
<213> Zea mays

<400> 118

cgccacgccg cctgcctgtc catgatctcc tgcgcgaact cggggtctac gagcaggctg 60

gcgaggcccg ggttcctgtc gtaggccttc ttgatgcggt ccaggaagat ggcgcggatg 120

atgcacccgc ccttccagat cctggccagc tcgccgaggt tgagccccca gcctttctcc 180

gcgctcttgg ccttgatgat gttcatgccc tgcgcgtagt gcagatcttg gacgcgtaca 240

gggcctgcct cacgtcctcc acca 264

<210> 119
<211> 254
<212> DNA
<213> Zea mays

<400> 119

cggacgcgtg gcggaccgtg gggacgtga ggcaagctct atatgcctcc aagatctgca 60

gttacgcgca aggcatgaac agcatcaagg ccaagagctc agagaaagga tggggcctca 120

accttggtga gctagcgagg atctggaagg gagggtgcat catccgtgcc atcttcctcg 180

accgcatcaa gaaggcgtac gataggaacc ctaaccttgc caacctcctc gttgaccccg 240

agttcgccca ggag 254

<210> 120
<211> 242
<212> DNA
<213> Zea mays

<400> 120

gcacgagctt ggactcgagg ttcctgagcg ggctgaagga cgagcgggtg gaggcctcca 60

agatcttcca gggtgactac tactccaccg gctcgccggt ggacaaggcg cactggtgga 120

ggacgtgagg caggccctgt acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat 180

catcaaggcc aagagcgcgg agaaaggctg gggctcaac ctcggcgagc tggccaggat 240

ct 242

<210> 121
<211> 225
<212> DNA
<213> Zea mays

<400> 121

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg 60

agaaaggctg gggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca 120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca 180

gcctgctcgt agaccccgag ttcgcgcagg agatcatgga caggc 225

<210> 122
<211> 220
<212> DNA
<213> Zea mays

<400> 122

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg 60

agaaaggctg gggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca 120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca 180

gcctgctcgt agaccccgag ttcgcgcagg agatcatgga 220

<210> 123
<211> 248
<212> DNA
<213> Zea mays

<400> 123

gtgcatcatc cgtgccatct tcctcgaccg catcaagaag gcgtacgata ggaaccctaa 60

ccttgccaac ctcctcgttg accccgagtt cgcccaggag atcatagaca ggcaagctgc 120

ctggcgcagg gttgtctgcc ttgccatcaa caatggcgtt agcaccccag gcatgtctgc 180

aagtctggcc tacttcgact cgtaccgaag agttaggttt cgcgaaactg tggtggaggc 240

tcagagag 248

<210> 124
<211> 209
<212> DNA
<213> Zea mays

<400> 124

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg 60

agaaaggctg gggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca 120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca 180

gcctgctcgt agaccccgag ttcgcgcag 209

<210> 125
<211> 210
<212> DNA
<213> Zea mays

<400> 125

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg 60

agaaaggctg gggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca 120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca 180

gcctgctcgt agaccccgag ttcgcgcagg 210

<210> 126
<211> 206
<212> DNA

<213>   Zea mays

<400>   126

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg 60

agaaaggctg gggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca 120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca 180

gcctgctcgt agaccccgag ttcgcg 206

<210>   127
<211>   176
<212>   DNA
<213>   Zea mays

<400>   127

gcgccatctt cctggaccgc atcaagaagg cctacgacag gaacccgggc ctcgccagcc 60

tgctcgtaga ccccgagttc gcgcaggaga tcatggacag gcaggcagcg tggcgcaggg 120

tggtgtgcct cgccatcaac aacggcgtca caccccggga atgtccgcta gcctgg 176

<210>   128
<211>   146
<212>   DNA
<213>   Zea mays

<400>   128

cgtgaggcag gccctgtacg cgtccaagat ctgcagctac gcgcagggca tgaacatcat 60

caaggccaag agcgcggaga aaggctgggg gctcaacctc ggcgagctgg ccaggatctg 120

gaagggcggg tgcatcatcc gcgcca 146

<210>   129
<211>   187
<212>   DNA
<213>   Zea mays

<400>   129

tggtggagga cgtgaggcag gccctgtacg cgtccaagat ctgcagctac gcgcagggca 60

tgaacatcat caaggccaag agcgcggaga aaggcttggg gctcggcctc ggcgagctgg 120

ccaggatctg gaagggcggg tgcatcatcc gcgccatctt cctggaccgc atcaagaatg 180

cctacga 187

<210> 130
<211> 123
<212> DNA
<213> Zea mays

<400> 130

gcctcaacct tggtgagcta gcgacgatct ggaaaggagg gtgcatcatc cgtgtaatct 60

tcctcgaccg catcaagaag gcgtacgata ggaaccctaa ccttgccaac ctcctcgttg 120

acc 123

<210> 131
<211> 83
<212> DNA
<213> Zea mays

<400> 131

gtgcatcatc cgtgccatct tcctcgaacg catcgagaag gcgtacgata ggaaccctaa 60

ccttgccaac ctcctcgttg acg 83

<210> 132
<211> 270
<212> DNA
<213> Zea mays

<400> 132

caggattctg gacaagactg ggatgaaggg gaccgggaaa tggaccgtgc agcaggcggc 60

ggacttgcgg tggcagcgcc acgattgccg cgtcgctgga cgggaggtac ctctcagggt 120

tgaaggacga acgggtcgca gccgctgggg tgctggagga agaggggatg ccggcagcct 180

gttggagacg gttaatgtcg acaagaaggt gctggtggat acggtcaggc aagcgctcta 240

cgcctccaag atttgcagct atgcgcaggg 270

<210> 133
<211> 258
<212> DNA
<213> Zea mays

<400> 133

cggacgcgtg ggggaaccgt gcagcaggcg gcggacttgc ggtggcagcg cccacgattg 60

ccgcgtcgca ggacgggagg tacctctcag ggttgaagga cgaacgggtc gcagccgctg 120

gggtgctgga ggaagagggg atgccggcag gcctgttgga gacggttaat gtcgacaaga 180

aggtgctggt ggatagggtc aggcaagcgc tctacgcctc caagatttgc agctatgcgc 240

agggaatgaa tctgctgc 258

<210> 134
<211> 119
<212> DNA
<213> Zea mays

<400> 134

atgcccggtg ttgactactc cagtcggtaa tgagatttcc tgcaggaact tgtctattga 60

tctttgtaag ttaattattt atatgaataa aataagagca aacatgcttg tgtttgggc 119

<210> 135
<211> 87
<212> DNA
<213> Zea mays

<400> 135

atgcccggtg ttgactactc cagtcggtaa tgagatttcc tgcaggaact tgtctattga 60

tctttgtaag ttaattattt atatgaa 87

<210> 136
<211> 312
<212> DNA
<213> Zea mays

<400> 136

atgtcctgga caagaccggg atgaatggaa ctgggaaatg gacagtccag caggctgctg 60

agctttctgt agctgctcct acaatcgagg cgtccttgga ctccaggttc ctcagcggtc 120

tgaaggacga gcgcgttgag gcttccaaaa tcttccaagg tgactactcc actggcctac 180

cggtggacaa ggcacagctg atcgaggacg tgaggcaagc tctatatgcc tccaagatct 240

gcagttacgc gcagggcatg aacatcatca aggccaagag ctcagagaaa ggatggggcc 300

tcaaccttgg tg 312

<210> 137
<211> 307
<212> DNA
<213> Zea mays

<400> 137

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tcgccgaggc ttatgatgtt ctcaagtcgg tgggtaagct cacaaacagc gagctgcatc 120

aggtgttctc tgagtggaac aagggtgagc tcctcagttt cttgattgag atcacggccg 180

acatctttgg tatcaaggat gacaagggtg aaggctacct ggtcgacaag gtcctggaca 240

agaccgggat gaagggaact gggaaatgga cagtccagca ggctgctgag ctttctgtag 300

ctgctcc 307

<210> 138
<211> 305
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 138

cgatatgcag ctgatttccg aggcttacga cgttctcaag tcggtcggta agctcaccaa 60

cagtgagctg caccaggtgt tctccgagtg gaacaagggg cgagctcctg agcttcttga 120

tcganatcac ggccgacatc tttggcatca aggacgagca tggcgatggc tacctagtgg 180

acaaggtcct tgacaagacc gggatgaaag ggacagggaa gtggacggtg cagcaggccg 240

ccgagctgtc ggtggccgct cctacgatcg angcgtcctt ggactcgagg ttcctgagcg 300

ggctg 305

<210> 139
<211> 356
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 139

tgttctcaag tcggtgggta agctaacaaa cagcgagctg catcaggtgt tctctgagtg 60

gaacaagggt gagctcctca gtttcttgat tgagatcacg gccgacatct ttggtatcaa 120

ggatgacaag ggtgaaggct acctggtcga caaggtcctg gacaagaccg ggatgaaggg 180

aactgggaaa tggacagtcc agcaggctgc tgagctttct gtagctgctc ctacaatcga 240

ggcgtccttg gactccaggt tcctcagcgg tctaaggacg agcgcgttga ggcttccana 300

atcttccaag gtgactactc cactgagcct acggtgngac aaggcacagc tgatcg 356

<210> 140
<211> 312
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 140

ctctgagtgg aacaagggtg agctcctcag tttcttgatt gagatcacgg ccgacatctt 60

tggtatcaag gatgacaagg gtgaaggcta cctggtcgac aaggtcctgg acaagaccgg 120

gatgaaggga actgggnaat ggacagtcca gcaagctgct gaacttcctg tagctgctcc 180

tacaatcaag gcgtccttgg actccaggtc cctcagcggt ctgaatgacg accgcgttga 240

ggcttccaaa atcttccaag gtgactactc cactggccta ccggtggaca aggcacagct 300

gatggaggac gt 312

<210> 141
<211> 275
<212> DNA
<213> Zea mays

<400> 141

gtggatcagg caactttgtc aagatggttc acaatgggat tgaatatggt gacatgcaac 60

ttatcgctga ggcttatgat gttctcaagt cggtgggtaa gctaacaaac agcgagctgc 120

atcaggtgtt ctctgagtgg aacaagggtg agctcctcag tttcttgatt gagatcacgg 180

ccgacatctt tggtatcaag gatgacaagg gtgaaggcta cctggtcgac aaggtcctgg 240

acaagaccgg gatgaaggga actgggaaat ggaca 275

<210> 142
<211> 268
<212> DNA
<213> Zea mays

<400> 142

tgttctccga gtggaacaag ggcgagctcc tgagcttctt gatcgagatc acggccgaca 60

tctttggcat caaggacgag catggcgatg gctacctggt ggataaggtc cttgacaaga 120

ccgggatgaa agggacaggg aagtggacgg tgcagcaggc cgccgagctg tcggtggccg 180

ctcctacgat cgaggcgtcc ttggactcga ggttcctgag cgggctgaag gacgagcggg 240

tggaggcctc caagatcttc cagggtga 268

<210> 143
<211> 269
<212> DNA
<213> Zea mays

<400> 143

cgacgttctc aagtcggtcg gtaagctcac caacagtgag ctgcaccagg tgttctccga 60

gtggaacaag ggcgagctcc tgagcttctt gatcgagatc acggccgaca tctttggcat 120

caaggacgag catggcgatg gctacctggt ggacaaggtc cttgacaaga ccgggatgaa 180

agggacaggg aagtggacgg tgcagcaggc cgccgagctg tcggtggccg ctcctacgat 240

cgaggcgtcc ttggactcga ggttcctga 269

<210> 144
<211> 267
<212> DNA
<213> Zea mays

<400> 144

ggcaaaggtg gatcgggcaa ctttgtcaag atggttcaca acggaatcga gtatggcgat 60

atgcagctga tttccgaggc ttacgacgtt ctcaagtcgg tcggtaagct caccaacagt 120

gagctgcacc aggtgttctc cgagtggaac aagggcgagc tcctgagctt cttgatcgag 180

atcacggccg acatctttgg catcaaggac gagcatggcg atggctacct agtggacaag 240

gtccttgaca agaccgggat gaaaggg 267

<210> 145
<211> 247
<212> DNA
<213> Zea mays

<400> 145

gagatcacgg ccgacatctt tggtatcaag gatgacaagg gtgaaggcta cctggtcgac 60

aaggtcctgg acaagaccgg gatgaaggga actgggaaat ggacagtcca gcaggctgct 120

gagctttctg tagctgctcc tacaatcgag gcgtccttgg actccaggtt cctcagcggt 180

ctgaaggacg agcgcgttga ggcttccaaa atcttccaag gtgactactc cactggccta 240

ccggtgg 247

<210> 146
<211> 265
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 146

cgtacnnttn gcanangtgg atcgggcaac tttgtcaaga tggtncacaa cggaatcgag 60

tatggcgata tgcagctgat ttccgangct tacgacgttc tcaagtcggt cggtaagctc 120

accaacagtg agnngcacca ngtgttctcc gantggaaca anggnnagct cctgngcttc 180

ttgatcgnga tnncggccga natcnttggc atcaaggacg agcatggcga tggctaccta 240

ntggncaagg tccntgacaa gaccg 265

<210> 147
<211> 216
<212> DNA
<213> Zea mays

<400> 147

gtccagcagg ctgctgagct ttctgtagct gctcctacaa tccaggcgtc cttggactcc 60

aggttcctca gcggtctgaa ggactagcgc gttgaggctt ccagaatctt ccaaggtgac 120

tactccactg gcctaccggt ggacaatgca cagctgatcg aggacgtgag gcaagctcta 180

tatgcctcca ggatctgcag ttacgcgcag ggcatg 216

<210> 148
<211> 256
<212> DNA
<213> Zea mays

<400> 148

caagggtgag ctcctcagtt tcttgattga gatcacggcc gacatctttg gtatcaagga 60

tgacaagggt gaaggctacc tggtcgacaa ggtcctggac aagaccggga tgaagggaac 120

tgggaaatgg acagtccagc aggctgctga gctttctgta gctgctccta caatcgaggc 180

gtccttggac tccaggttcc tcaccgtctt aaaggacgac cgcgttgagg cttccaaaat 240

cttccaaggt ggatat 256

<210> 149
<211> 176
<212> DNA
<213> Zea mays

<400> 149

aaacagcgag ctgcatcagg tgttctctga gtggaacaag ggtgagctcc tcagtttctt 60

gattgagatc acggccgaca tctttggtat caaggatgac aagggtgaag gctacctggt 120

cgacaaggtc ctggacaagc cgggatgaag ggaactggga aatggacact ccaaca 176

<210> 150
<211> 185
<212> DNA
<213> Zea mays

<400> 150

cgacgttctc aagtcggtcg gtaagctcac caacagtgag ctgcaccagg tgttctccga 60

gtggaacaag ggcgagctcc tgagcttctt gatcgagatc acggccgaca tctttggcat 120

caaggacgag catggcgatg gctacctggt ggacaaggtc cttgacaaga ccgggatgaa 180

aggga 185

<210> 151
<211> 136
<212> DNA
<213> Zea mays

<400> 151

caaacagcga gctgcatcag gtgttctctg agtggaacaa ggggcggctc ctcagtttct 60

tgattgagat cacggccgac atctttggta tcaaggatga caagggtgaa ggctacctgg 120

tcgacaaggt cctgga 136

<210> 152
<211> 282
<212> DNA
<213> Zea mays

<400> 152

cggcgctcac acgtacgaga gggacaggct tcccgccaac ctggtgcagg ctcagagaga 60

ctacttcggc gctcacacgt acgagagggt tgacatgcct ggttctttcc acaccgagtg 120

gttcaagatt gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta 180

tgccaccgtg tcgagtaatc actcatatta ctgcttgcag ggaggaactg tgtttgattt 240

ttattttcca tgcgcaatgc ttaatttagg tcaggaagtc ca 282

<210> 153
<211> 248
<212> DNA
<213> Zea mays

<400> 153

gcacgagcag ggataggctt cccgccaacc tggtgcaggc tcagagagac tacttcggcg 60

ctcacacgta cgagagggtt gacatgcctg gttctttcca caccgagtgg ttcaagattg 120

cgcgcaactc caagatctga acatggcctc gtgtttgcat atgccagtat gccaccgtgt 180

cgagtaatca atcatattac tgcttgcagg gaggaactgt gtttgatttt tattttccat 240

gcgcaatg 248

<210> 154
<211> 254
<212> DNA
<213> Zea mays

<400> 154

gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta tgccaccgtg 60

tcgagtaatc aatcatatta ctgcttgcag ggaggaactg tgtttgattt ttattttcca 120

tgcgcaatgc ttaatttagg tcaggaagtc caaagtctct cccattgttt tcctgtaaga 180

gctaagcagt accagatgga gaaccttata tttgctggaa catgaataga agcatttgac 240

atgcttgtgc ttac 254

<210> 155
<211> 236
<212> DNA
<213> Zea mays

<400> 155

gcacgagatt gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta 60

tgccaccgtg tcgagtaatc aatcatatta ctgcttgcag ggaggaactg tgtttgattt 120

ttattttcca tgcgcaatgc ttaatttagg tcaggaagtc caaagtctct cccattgttt 180

tcctgtaaga gctaagcagt accagatgga gaaccttata tttgctggaa catgaa 236

<210> 156
<211> 197
<212> DNA
<213> Zea mays

<400> 156

agacaggcaa gctgcctggc gcagggttgt ctgccttgcc atcaacaatg gcgttagcac 60

cccaggcatg tctgcaagtc tggcctactt cgactcgtac cgcagggaca ggcttcccgc 120

caacctggtg caggctcaga gagactactt cggcgctccc acgtacgaga gggttgacat 180

gcctggttct ttccaca 197

<210> 157
<211> 281
<212> DNA
<213> Zea mays

<400> 157

cggacgcgtg ggcggacgcg tgggcggacg cgtgggggca agctgcctgg cgcagggttg 60

tctgccttgc cactcaacaa tggcagttac accccaggca tgtctgcaca gtctggccta 120

cttcgactcg taccgcagga caggcttccc gccaacctgg tgcaggctca gagagactac 180

ttcggcgctc acacgtacga gagggttgac atgcctggtt ctttccacac cgagtggttc 240

aagattgcgc gcaactccaa gatctgaaca tggcctcgtg t 281

<210> 158
<211> 249
<212> DNA

<213>	Zea mays

<400>	158

cttgccatca acaatggcgt tacaccccag gcatgtctgc aagtctggcc tacttcgact	60

cgtaccgcag gacaggcttc ccgccaacct ggtgcaggct cagagagact acttcggcgc	120

tcacacgtac gagagggttg acatgcctgg ttctttccac accgagtggt tcaagattgc	180

gcgcaactcc aagatctgaa catggcctcg tgtttgcata tgccagtatg ccaccgtgtc	240

gagtaatca	249

<210>	159
<211>	150
<212>	DNA
<213>	Zea mays

<400>	159

gggaggaact gtgtttgatt tttattttcc atgcgcaatg cttaatttag gtcaggaagt	60

ccaaagtctc tcccattgtt ttcctgtaag agctaagcag taccagatgg agaaccttat	120

atttgctgga acatgaataa aagcatttga	150

<210>	160
<211>	133
<212>	DNA
<213>	Zea mays

<400>	160

gtaagtctgg cctacttcga ctcgtaccgc agggacaggc ttcccgccaa cctggtgcag	60

gctcagagag actacttcgg cgctcacacg tacgagaggg ttgacatgcc tggttctttc	120

cacaccgaat ggt	133

<210>	161
<211>	72
<212>	DNA
<213>	Zea mays

<400>	161

attgcgcgca actccaagat ctgaacatgg cctcgtgttt gcatatgcca gtatgccacc	60

gtgtcgagta at	72

<210> 162
<211> 327
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 162

atcaggggga ctgtatcgtc gatggtggca acgagtggta cgagaacacg gagaggaggg 60

agaaggcgat ggaggagcgc gggctcctat atcttggcat gggcgtctcc ggaggagagg 120

agggtgcccg caatggcccg tccttgatgc ccgggggctc cttcgaggca tacaagtaca 180

ttgaagatat tcttctcaag gtggctgctc aggtacctga cagcggcccg tgcgtcacat 240

atattggcaa aagtggatca ggcaacttcg tcaagatggt tcacaatgga attgaatatg 300

gtgacatgcn acttatcgcc gaggctt 327

<210> 163
<211> 331
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 163

cgagtggtac gagaacacgg agaggangga gaaggcgatg gaggagcgcg ggctcctata 60

tcttggcatg ggcgtctccg gaggagagga nggtgcccgc aatggcccgt ccttgatgcc 120

cgggggctcc ttcgaggcat acaagtacat tgaagatatt cttctcaagg tggctgctca 180

ggtacctgac agcggcccgt gcgtcacata tattggcaaa ggtggatcag gcaactttgt 240

caagatggtt cacaatggga ttgaatatgg tgacatgcaa cttatcgctg aggcttatga 300

tgttctcaag tcggtgggta actaacaaac a 331

<210> 164
<211> 297
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 164

cacggagagg agggagaagg ccatggagga gcgcggcctc ctgtatcttg gcatgggtgt 60

ctctggagga gagganggtg cccgcaacgg cccgtccttg atgcccggag gctcgttcga 120

ggcttacaag tacgtcgaag acattgtcct caaggtggct gctcaggtcc ctgacagtgg 180

cccgtgtgtc acgtacattg gcaaaggtgg atcgggcaac tttgtcaaga tggttcacaa 240

cggaatcgag tatggcgata tgcagctgat ttccgaggca tacgacgttc tcaagtc 297

<210> 165
<211> 324
<212> DNA
<213> Zea mays

<400> 165

ggtggccgga cggtggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag 60

cgcgccagtc catagtgtag gaggaggaga tggcgctcac aagaatcggt cttgctggcc 120

ttgcggtcat ggggcagaac ccttgcctca agcattgcag agaaagggtt ccccatctct 180

gtgtacaaca ggacaacctc caaggtggac gagaccgtgc agcgtgccaa ggcagaagga 240

aaccttcccg tctacggctt ccatgacccc gcgtcctttg tgaactccat tcagaagcca 300

cgggtggtga tcatgctcgt caag 324

<210> 166
<211> 287
<212> DNA
<213> Zea mays

<400> 166

gccacgggtg gtgatcatgc tcgtcaaggc cggcgacaca gttgtgcaga ccatcgcgac 60

gctcgcagct cacttggagc agggcgactg cgtcatcgat gggggggaacg agtggtacga 120

gaacacggag aggagggaga aggccatgga ggagcgcggc ctcctgtatc ttggcatggg 180

tgtctctgga ggagaggagg gtgcccgcaa cggcccgtcc ttgatgcccg gaggctcgtt 240

cgaggcttac aagtacgtcg aagacattgt cctcaaggtg gctgctc 287

<210> 167
<211> 283
<212> DNA
<213> Zea mays

<400> 167

ccgcatctga atcggcactc ggcagcgcgc cactccatag tgtaggagga gatggcgctc 60

acaagaatcg gtcttgctgg ccttgcggtc atggggcaga accttgccct caacattgca 120

gagaaagggt tccccatctc tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg 180

cagcgtgcca aggcagaagg aaaccttccc gtctacggct tccatgaccc cgcgtccttt 240

gtgaagtcca ttcagaagcc acgggtggtg atcatgctcg tca 283

<210> 168
<211> 285
<212> DNA
<213> Zea mays

<400> 168

ggtggacgag accgtgcagc gtgccaaggc agaaggaaac cttcccgtct acggcttcca 60

tgaccccgcg tcctttgtga agtccattca gaagccacgg gtggtgatca tgctcgtcaa 120

ggccggcgcg ccagttgacc agaccatcgc gacgctcgca gctcacttgg agcagggcga 180

ctgcatcatc gatgggggga acgagtggta cgagaacacg gagatgaggg agaaggccat 240

ggaggatcgc ggcctcctgt atcttggcat gggtgtctct ggagg 285

<210> 169
<211> 311
<212> DNA
<213> Zea mays

<400> 169

gccggaggtg gtggcatcgc aattcaactc cgcatctgaa tcggcactcg gcagcgcgcc 60

actccatagt gtaggaggag gagatggcgc tcacaagaat cggtcttgct ggccttgcgg 120

tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc tctgtgtaca 180

acaggacaac ctccaaggtg gacgagaccg tgcagcgtgc caaggcagaa ggaaaccttc 240

ccgtctacgg cttccatgac cccgcgtcct ttgtgaactc cattcagaag ccacgggtgg 300

tgatcatgct c 311

<210> 170
<211> 290
<212> DNA
<213> Zea mays

<400> 170

aattcaactc cgcatctgaa tcggcactcg gcagcgcgcc agctccatag cgaggagatg 60

gcgctcacaa gaatcggtct tgctggcctt gcggtcatgg ggcagaacct tgccctcaac 120

attgcagaga tagggttccc catctctgtg tacaacagga caacctccaa ggtggacgag 180

accgtgcagc gtgccaaggc agaaggaaac cttcccgtct acggcttcca tgaccccgcg 240

tcctttgtga agtccattca gaagccacgg gtggtgatca tgctcgtcaa 290

<210> 171
<211> 275
<212> DNA
<213> Zea mays

<400> 171

gccacgggtg gtgatcatgc tcgtcaaggc cggcgcgcca gttgaccaga ccatcgcgac 60

gctcgcagct cacttggagc agggcgactg catcatcgat gggggggaacg agtggtacga 120

gaacacggag aggagggaga aggccatgga ggagcgcggc ctcttgtatc ttggcatggg 180

tgtctctgga ggagaggagg gtgcccgcaa cggcccgtcc ttgatgcccg gatgctcgtt 240

cgacgcttac aagtacgtcg aagacattgt tctca 275

<210> 172
<211> 296
<212> DNA
<213> Zea mays

<400> 172

gagaggtagg tggccggacg gtggtggcat cgccaattca actccgcatc tgaatcggca 60

ctcggcagcg cgccactcca tagtgtagga ggaggagatg gcgctcacaa gaatcggtct 120

tgctggcctt gcggtcatgg ggcagaacct tgccctcaac attgcagaga aagggttccc 180

catctctgtg tacaacagga caacctccaa ggtggacgag accgtgcagc gtgccaaggc 240

agaaggaaac cttcccgtct acggcttcca tgaccccgcg tcctttgtga actcca 296

<210> 173
<211> 268
<212> DNA
<213> Zea mays

<400> 173

gcgactgcat catcgatggg gggaacgagt ggtacgagaa cacggagagg agggagaagg 60

ccatggagga gcgcggcctc ttgtatcttg gcatgggtgt ctctggagga gaggagggtg 120

cccgcaacgg cccgtccttg atgcccggag gctcgttcga cgcttacaag tacgtcgaag 180

acattgttct caaggtggct gctcaggtcc ctgacagtgg cccgtgtgtc acgtacattg 240

gcaaaggtgg atcgggcaac tttgtcaa 268

<210> 174
<211> 276
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 174

acaagtacat tgaagatatt cttctcaagg tggctgctca ggtacctgac agcggcccgt 60

gcgtcacata tattggcaaa ggtggatcag gcaacttcgt caagatggtt cacaatggaa 120

ttgaatatgg tgacatgcaa cttatcgccg aggcttatga tgttctcaag ttcggtgggt 180

aagctcacaa acngcgagct gcatcaggtg ttctctgagt ggaacaaggg tgagctcctc 240

agtttcttga ttgagatcac ggccgacatc ttggta 276

<210> 175
<211> 297
<212> DNA
<213> Zea mays

<400> 175

gtaggtggcc ggacggtggt gggctcgcca attcaactcc gcatctgaat cggcactcgg 60

cagcgcgcca gctccatagt gtaggaggag gtgatggcgc tcacaagaat cggtcttgct 120

ggccttgcgg tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc 180

tctgtgtaca acaggacaac ctccaaggtg gacgagaccg tgcagcgtgc caaggcagaa 240

ggaaaccttc ccgtctacgg cttccatgac cccgcgtcct ttgtgaactc cattcag 297

<210> 176
<211> 274
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 176

acaagtacat tgaagatatt cttctcaagg tggctgctca ggtacctgac agcggcccgt 60

gcgtcacata tattggcaaa ggtggatcag gcaacttcgt caagatggtt cacaatggaa 120

ttgaatatgg tgacatgcaa cttatcgccg aggcttatga tgttctcaag tccggtgggt 180

aagctcacaa acngcgagct gcatcaggtg ttctctgagt ggaacaaggg tgagctcctc 240

agtttctgat tgagatcacg gccgacatct tggt 274

<210> 177
<211> 274
<212> DNA
<213> Zea mays

<400> 177

ggtggccgga cggtggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag 60

cgcgccactc catagtgtag gaggagatgg cgctcacaag aatcggtctt gctggccttg 120

cggtcatggg gcagaacctt gccctcaaca ttgcagagaa agggttcccc atctctgtgt 180

acaacaggac aacctccaag gtggacgaga ccgtgcagcg tgccaaggca gaaggaaacc 240

ttcccgtcta cggcttccat gaccccgcgt cctt 274

<210> 178
<211> 271
<212> DNA
<213> Zea mays

<400> 178

cggtggccgg acggtggtgg catcgccaat tcaactccgc atctgaatcg gcactcggca 60

gcgcgccact ccatagtgta ggaggaggag atggcgctca caagaatcgg tcttgctggc 120

cttgcggtca tggggcagaa ccttgccctc aacattgcag agaaagggtt ccccatctct 180

gtgtacaaca ggacaacctc caaggtggac gagaccgtgc agcgtgccaa ggcagaagga 240

aaccttcccg tctacggctt ccatgacccc g 271

<210> 179
<211> 258
<212> DNA
<213> Zea mays

<400> 179

gggttcccca tctctgtgta caacaggaca acctccaagg tggacgagac cgtgcagcgt 60

gccaaggcag aaggaaacct tcccgtctac ggcttccatg accccgcgtc ctttgtgaac 120

tccattcaga agccacgggt ggtgatcatg ctcgtcaagg ccggcgcgcc agttgaccag 180

atcatcgcga cgctcgcagc tcacttggag cagggcgact gcatcatcga tgggggaac 240

gagtggtacg agaacacg 258

<210> 180
<211> 270
<212> DNA
<213> Zea mays

<400> 180

ggccggcgcg ccagttgacc agaccatcgc gacgctcgca gctcacttgg agcagggcga 60

ctgcatcatc gatgggggga acgagtggta cgagaacacg gagaggaggg agaaggccat 120

ggaggagcgc ggcctcttgt atcttggcat gggtgtctct ggaggagagg agggtgcccg 180

caacggcccg tccttgatgc ccggaggtcg ttcgacgctt acaagtacgt cgagacattg 240

ttctcaaggt ggctgctcag gtccctgaca 270

<210> 181
<211> 251
<212> DNA
<213> Zea mays

<400> 181

gtgatcatgc tcgtcaaggc cggcgcgcca gtagaccaga ccatcgcgac gctcgcagct 60

cacttggagc agggcgactg catcatcgat gggggaacg agtggtacga gaacacggag 120

aggagggaga aggccatgga ggagcgcggc ctcttgtatc ttggcatggg tgtctcttga 180

ggagaagaag gtgcccgcaa cggcccgtcc ttgatgcccg ggagctcgtt cgacgcttac 240

aagtacgtcg a 251

<210> 182
<211> 224
<212> DNA
<213> Zea mays

<400> 182

gccggaggtg gtggcatcgc caattcaact ccgcatctga atcggcactc ggcagcgcgc 60

cagctccata gtgtaggagg agatggcgct cacaagaatc ggtcttgctg gccttgcggt 120

catggggcag aaccttgccc tcaacattgc agagaaaggg ttccccatct ctgtgtacaa 180

caggacaacc tccaaggtgg acgagaccgt gcagcgtgcc aagg 224

<210> 183
<211> 233
<212> DNA
<213> Zea mays

<400> 183

gccggaggtg gtggcatcgc caattcaact ccgcatctga atcggcactc ggcagcgcgc 60

cactccatag tgtaggagga ggagatggcg ctcacaagaa tcggtcttgc tggccttgcg 120

gtcatggggc agaaccttgc cctcaacatt gcagagaaag ggttccccat ctctgtgtac 180

aacaggacaa cctccaaggt ggacgagacc gtgcagcgtg ccaaggcaga agg 233

<210> 184
<211> 235
<212> DNA
<213> Zea mays

<400> 184

ggccggacgg tggtggcatc gccaattcaa ctccgcatct gaatcggcac tcggcagcgc 60

gccagtccat agtgtatgag gagatggcgc tcacaagaat cggtcttgct ggccttgcgg 120

tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc tctgtgtaca 180

acaggacaac ctccaaggtg gacgagaccg tggcacgtgc caaggcagaa ggaaa 235

<210> 185
<211> 263
<212> DNA
<213> Zea mays

<400> 185

cttccctgcc cgattggcga tttaagtggt gggggaggga aggacgatgg tcagtgaaag 60

agaggtaggt ggccggacgg tggtggcatc gccaattcaa ctccgcatct gaatcggcac 120

tcggcagcgc gccagctcca tagtgtagga ggagatggcg ctcacaagaa tcggtcttgc 180

tggccttgcg gttatggggc agaaccttgc cctcaacatt gcagagaaag ggttccccat 240

ctctgtgtac aacaggacaa cct 263

<210> 186
<211> 221
<212> DNA
<213> Zea mays

<400> 186

ggccggacgg tggtggcatc gccaattcaa ctccgcatct gaatcggcac tcggcagcgc 60

gccagctcca taggaggagg agatggcgct cacaagaatc ggtcttgctg gccttgcggt 120

catggggcag aaccttgccc tcaacattgc agagaaaggg ttccccatct ctgtgtacaa 180

caggacaacc tccaaggtgg acgagaccgt gcaaggtgcc a 221

<210> 187
<211> 294
<212> DNA
<213> Zea mays

<400> 187

cccgaaagcc gccaagcggc tgctgcgcaa ggagcgaaag gcacttccct acccgattgg 60

cgatttaagt ggtgggggag ggaaggccga tggtcagtga aagagaggta ggtggccgga 120

cggaggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag cgcgccagca 180

ccataggagg agatggcgct cacaagaatc ggtcttgctg gccttgcggt catggggcag 240

aaccttgccc tcaacattgc agagaaaggg ttcccgatct ctgtgtacaa cagg 294

<210> 188
<211> 200
<212> DNA
<213> Zea mays

<400> 188

ggccggacgg tggtggcatc gccaattcaa ctccgcatct gaatcggcac tcggcagcgc 60

gccagctcca taggaggagg agatggcgct cacaagaatc ggtcttgctg gccttgcggt 120

catgtggcag aaccttgccc tcaacattgc agagaaaggg ttccccatct ctgtgtacaa 180

caggacaacc tccaaggtgg 200

<210> 189
<211> 154
<212> DNA
<213> Zea mays

<400> 189

ctccgcatct gcatcggcag cgcgccagct ccataggagg agatggcgct cacaagaatc 60

ggtcttgctg gccttgcggt catggggcag aaccttgccc tcaacattgc agagaaaggg 120

ttccccatct ctgtgtacaa caggacaacc tcca 154

<210> 190
<211> 127
<212> DNA
<213> Zea mays

<400> 190

ggtaggtggc cggacggtgg tggcatcgcc agttcaactc cgcatctgaa tcggcactcg 60

gcagcgcgcc actccatagg aggagatggc gctcacaaga atcggtcttg ctggccttgc 120

ggtcatg 127

<210> 191
<211> 104
<212> DNA
<213> Zea mays

<400> 191

gccggacggt ggtggcatcg ccaattcaac tccgcatctg aatcggcact cggcagcgcg 60

ccagctccat agtgtaggag gagatggcgc tcacaagaat cggt 104

<210> 192
<211> 162
<212> DNA
<213> Zea mays

<400> 192

ggcaccttcc ctgccccgatt ggcgatttaa gtggtggggg agggaaggcc gatggtcagt 60

gaaagagagg taggtggccg gacggtggtg gcatcgccaa ttcaactccg catctgaatc 120

ggcactcggc agcgcgccag ctccatagtg atagaggagg ag 162

<210> 193
<211> 87
<212> DNA
<213> Zea mays

<400> 193

gcatacaagt acattgaaga tattcttctc aaggtggctg ctcaggtacc tgacagcggc 60

cgtgcgtcac atatatggca aggtgga 87

<210> 194
<211> 91
<212> DNA
<213> Zea mays

<400> 194

cgggtggctg ctcaggtacc tgaccgcggc ccgtgcgtca catatattgg caaaggtgcc 60

tcaggcaact tcgtcaagat ggttcacaat c 91

<210> 195
<211> 330
<212> DNA
<213> Zea mays

<400> 195

ccgcgctgca ggggcgacgc aaggccgagc gctcctcgat ccagatccaa ggtaggagat 60

ggctctcacg agaattggcc tcgccggcct cgcggtcatg ggacagaacc ttgccctcaa 120

catcgcggag aaagggttcc ccatctcggt ctacaacagg acaacctcca aggttgatga 180

gaccgtgcag cgtgccaagg tcgaaggaaa cctcccagtg tttggtttcc acgaccccgc 240

gtccttcgtg agctccatcc agaagccccg tgtcgtcatc atgctcgtca aggctggggc 300

gccggtggac cagaccattg ccacgctcgc 330

<210> 196
<211> 323
<212> DNA
<213> Zea mays

<400> 196

tccagatcca aggtaggaga tggctctcac gagaattggc ctcgccggcc tcgcggtcat 60

gggacagaac cttgccctca acatcgcgga gaaagggttc cccatctcgg tctacaacag 120

gacaacctcc aaggttgatg agaccgtgca gcgtgccaag gtcgaaggaa acctcccagt 180

gtttggtttc cacgaccccg cgtccttcgt gagctccatc cagaagcccc gtgtcgtcat 240

catgctcgtc aaggctgggg cgccggtgga ccagaccatt gccacgctcg cggcgcacct 300

tgatcagggg gactgtatcg tcg 323

<210> 197
<211> 350
<212> DNA
<213> Zea mays

<400> 197

agcgtgccaa ggtcgaagga aacctcccag tgtttggttt ccacgacccc gcgtccttcg 60

tgagctccat ccagaagccc cgtgtcgtca tcatgctcgt caaggctggg gcgccggtgg 120

accagaccat tgccacgctc gcggcgcacc ttgatcaggg ggactgtatc gtcgatggtg 180

gcaacagtgg tacgagaaca cggagaagag ggagaaggcg atggaagagc gcgggctcct 240

atatcttggc atgggcgtct ccggaggaga ggacggtgcc cgcaatggct cgtccttgat 300

gcccgggggc tccttcgagg catacaagta cattgaagat attcttctca 350

<210> 198
<211> 317
<212> DNA
<213> Zea mays

<400> 198

gcaaggccga gcgctcctcg atccagatcc aaggtaggag atggctctca cgagaattgg 60

cctcgccggc ctcgcggtca tgggacagaa ccttgccctc aacatcgcgg agaaagggtt 120

ccccatctcg gtctacaaca ggacaacctc caaggttgat gagaccgtgc agcgtgccaa 180

ggtcgaagga aacctcccag tgtttggttt ccacgacccc gcgtccttcg tgagctccat 240

ccagaagccc cgtgtcgtca tcatgctcgt caaagctggg gcgccggtgg accagaccat 300

tgccacgctc gcggcgc 317

<210> 199
<211> 299
<212> DNA
<213> Zea mays

<400> 199

ctctcgcctc ggcttggcag tcggcactcc ctctccaccg cgctgcaggg gcgacgcaag 60

gccgagcgct cctcgatcca gatccaaggt aggagatggc tctcacgaga attggcctcg 120

ccggcctcgc ggtcatggga cagaaccttg ccctcaacat cgcggagaaa gggttcccca 180

tctcggtcta caacaggaca acctccaagg ttgatgagac cgtgcagcgt gccaaggtcg 240

aaggaaacct cacagtgttt ggtttccacg accccgcgtc cttcgtgagc tccatccag 299

<210> 200
<211> 279
<212> DNA
<213> Zea mays

<400> 200

tgtcggcact ccctctccac cgcgctgcag ggcgacgca aggccgagcg ctcctcgatc 60

cagatccaag gtaggagatg gctctcacga gaattggcct cgccggcctc gcggtcatgg 120

gacagaacct tgccctcaac atcgcggaga aagggttccc catctcggtc tacaacagga 180

caacctccaa ggttgatgag accgtgcagc gtgccaaggt cgaaggaaac ctcccagtgt 240

ttggtttcca cgaccccgcg tccttcgtga gctccatcc 279

<210> 201
<211> 321
<212> DNA
<213> Zea mays

<400> 201

gtaggctggc gctgcagatc aaaaggctct cgcctcggct tggcagtcgg cactccctct 60

ccaccgcgct gcaggggcga cgcaaggccg agcggtcctc gatccaggtc caaggtagga 120

gatggctctc acgaggaatg gcctcgccgg cctcgcggtc atgggacaga accttgccct 180

caacatcgcg gagaaagggt tccccatctc ggtctacaac aggacaacct ccaaggttga 240

tgagaccgtg cagcgtgcca aggtcgaaag aaacctccca gtgtttggtt tccacgaccc 300

cgcgtccttc gtgagctcca t 321

<210> 202
<211> 267
<212> DNA
<213> Zea mays

<400> 202

cccatctcgg tctacaacag gacgacctcc aaggttgatg agaccgtgca gcgtgccaag 60

gtcgaaggaa acctccccgt gtttggtctc cacgaccccg cgtccttcgt gagctccatc 120

cagaagcccc gtgtcgtcat catgctcgtc aaggctgggg cgccggtgga ccagaccatt 180

gccacgctcg cggcgcacct ggatcagggg gactgtatcg tcgatggtgg caacgagtgg 240

tacgagaaca cggagaggaa ggagaag 267

<210> 203
<211> 266
<212> DNA
<213> Zea mays

<400> 203

gctgcagatc aaaaggctct cgcctcggct tggcagtcgg cactccctct ccaccgcgct 60

gcaggggcga cgcaaggccg agcgctcctc gatccagatc caaggtagga gatgtgtctc 120

acgagaattg gcctcgccgg cctcgcggtc atgggacaga accttgccct caacatcgcg 180

gagaaagggt tccccatctc ggtctacaac aggacgacct ccaaggttgg gaagaccgtg 240

cagcgtgcca aggtcgaagg aaacct 266

<210> 204
<211> 264
<212> DNA
<213> Zea mays

<400> 204

cgctgcagat caaaaggctc tcgcctcggc ttggcagtcg gcactccctc tccaccgcgc 60

tgcaggggcg acgcaaggcc gagcgctcct cgatccagat ccaaggtagg agatggctct 120

cacgagaatt ggcctcgccg gcctcgcggt catgggacag aaccttgccc tcaacatcgc 180

ggagaaaggg ttccccatct cggtctacaa caggacaacc tccaaggttg atgagaccgt 240

gcagcgtgcc aaggtcgaag gaaa 264

<210> 205
<211> 294
<212> DNA
<213> Zea mays

<400> 205

aacgtaggct ggcgctgcag atcaaaaggc tctcgcctcg gcttggcagt cggcactccc 60

tctccaccgc gctgcagggg cgacgcaagg ccgagcgctc ctcgatccag atccaaggta 120

ggagatggct ctcacgagaa tgcgcctcgc cggcctcgcg gtcatgggac agaaccttgc 180

cctcaacatc gcggagaaag ggttccccat ctcggtctac aacaggacaa cctccaaggt 240

tgatgagacc gtgcagcgtg ccaaggtcga aggaaacctc ccagtgtttg gttt 294

<210> 206
<211> 150
<212> DNA
<213> Zea mays

<400> 206

cagaactccg tgtcgtcata tgctcgtcaa ggctggggcg ccggtggacc agaccattgc 60

cacgctcgcg gcgcaccttg atcaggggga ctgtatcgtc gatggtggca acgagtggta 120

cgagaacacg gagaggaggg agaaggcgat 150

<210> 207
<211> 161
<212> DNA
<213> Zea mays

<400> 207

caaaaggctc tcgcctcggc ttggcagtcg gcactccctc tccaccgcgc tgcaggggcg 60

acgcaaggcc gagcgctcct cgatccagat ccaaggtagg agatggctct cacgagaatt 120

ggcctcgccg gcctcgcggt catgggacag aaccttgccc t 161

<210> 208
<211> 161
<212> DNA
<213> Zea mays

<400> 208

caaaaggctc tcgcctcggc ttggcagtcg gcactccctc tccaccgcgc tgcaggggcg 60

acgcaaggcc gagcgctcct cgatccagat ccaaggtagg agatggctct cacgagaatt 120

ggcctcgccg gcatcgcggt catgggacag aaccttgccc t 161

<210> 209
<211> 205
<212> DNA
<213> Zea mays

<400> 209

accttgccct caacatcgcg gagaaagggt tccccatctc ggtctacaac aggacgacct 60

ccaaggttga tgagaccgtg cagcgtgcca aggtcgaagg aaacctcccc gtgtttggtt 120

tccacgaccc cgcgtccttc gtgagctccc atccagaagc cccgtgtcgt catcatgctc 180

gtcaaggctg gggcgccggt ggacc 205

<210> 210
<211> 270
<212> DNA
<213> Glycine max

<400> 210

ggccggcgcc cccgtcgacc aaaccatcgc cgccctctcc gaccacctcg accccggcga 60

ctgcatcatc gacggcggca acgagtggta cgagaacacc gagcgccgca tgagcctcgt 120

cgccgacaaa ggcctcctct acctcggcat gggcgtctcc ggcggcgaag acggcgcacg 180

ccacggcccc tccctcatgc ccggtgggtc ccaccaggcc tactccaacg tccaggacat 240

cctccacaaa atcgccgccc aggtcgacga 270

<210> 211
<211> 165
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 211

angagtgnnt acgagaacac cgagcgccgc atgaacctcg tcgccgacaa aggcctcctc 60

tanctcggca tgggcgtctc cggcggcgaa gacggcgcac gccacggccc ctccctcatg 120

cccggtgggt cccaccatgc ctactccaac gtgccagnac atcct 165

<210> 212
<211> 248
<212> DNA
<213> Glycine max

<400> 212

ggcgtatgca agggaaatgg tgtatagaca ggctgcgtgg catagaatcg tggggttggc 60

ggtttcggct gggattagta ctagcggaat gtgtgccagt cttgcttggt ttgataccta 120

tcggagggca agacttccgg caaaccttgt ccaggctcag agggacttgt ttggggcgca 180

tacttacgag agggttgatc gccctggggc ttttcatacc gagtggacga aactcgctcg 240

caatagtg 248

<210> 213
<211> 251
<212> DNA
<213> Glycine max

<400> 213

ggagtttgca agggaaatgg tgcagagaca ggctgcgtgg atgagggttg tggggttggc 60

ggtttcggct gggattagta ctcccggaat gtgtgccagt cttgcttact ttgataccta 120

tcggagggca agacttccgg caaaccttgt ccaggctcag agggacttgt ttggggcgca 180

tacttacgag agggttgatc gccctggggc ttttcatacc gagtggacga aactcgctcg 240

caatagtggg g 251

<210> 214
<211> 272
<212> DNA
<213> Glycine max

<400> 214

gataagaagc agttgatcga tgacgtcagg caggctctga atgcttccaa gattagcagt 60

tatgctcagg ggatgaattt gttgagggct aagagtaatg agaaaggatg gaacttgaat 120

ttgggggagt tagctaggat tggaagggag ggtgcatcat aagggccgtg ttcttggacc 180

ggatcaagaa ggcttatcag aggaacccta atttggcgag tttgattgtg gacccggagt 240

atgcaaggcg aatagtccag agacacgctg cg 272

<210> 215
<211> 196
<212> DNA
<213> Zea mays

<400> 215

gccacgcgtc cgcggacgcg tggattccat gtgagggcat cagctcgggt tgacaaattc 60

tcaaagagtg acatcatcgt gtccccttcg attctgtctg caaactttgc gaagcttggt 120

gatcaggtaa aagctgtgga ggtggcagga tgcgactgga ttcatgtcga tgtcatggac 180

gggcgctttg tgccaa 196

<210> 216
<211> 353
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 216

tgcgtcatct acgcgcagga aggcgttcca agtgagggca tcagctcggg ttgacaagtt 60

ctcaaagagt gatatcaggg tngtcccttc gcatctgtct ggaaactgtc gcaaagctat 120

gttgatcagg tagaagcgtg ggaggtggca agatgtgact ggattctgtc gatgtcatgg 180

acgggcgctg tgtgcgaaat atcacaattg gacctgtggt tgttgatgct ctgcgtcctg 240

tgactgatct tccattggat gtacatctga tgattgtgga acctgagcag cgagtcactg 300

attgtatcaa ggcangtgct gatattgtta gtgtccactg tgaacagaca tcg 353

<210> 217
<211> 312
<212> DNA
<213> Zea mays

<400> 217

agcgactcca ctcactgcaa ttgattatgt tcttgatgtt gttgacctgg tgctgattat 60

gtctgtgaat cctgggtttg gtggccagag ctttatcgag agtcaagtaa agaaaattgc 120

agaactgaga aggttatgtg cagagaaggg agtgaacccc tggattgagg ttgatggtgg 180

tgttggtccg aaaaatgcct acaaggttat tgaagctggc gcaaatgcca ttgtcgcagg 240

ttctgcagtt tttggggctc cagactacgc tgaagctatc aaaggaataa agaccagcca 300

aagacctcta gc 312

<210> 218
<211> 312
<212> DNA
<213> Zea mays

<400> 218

gctctgcgtc cagtgactga tcttccgttg gatgtacatc tgatgattgt ggaacctgag 60

cagcgagtcc ccgattttat caaggcaggt gctgatattg ttagtgtcca ctgtgaacag 120

acatcgacca tccatttgca ccgaacagtc aatcagatta aaagtctagg agcaaaggca 180

ggagttgttt tgaatccagc gactccactc actgcaattg attatgttct tgatgttgtt 240

gacctggtgc tgattatgtc tgtgaatcct gggtttggtg gccagagctt tatcgagagt 300

caagtaaaga aa 312

<210> 219
<211> 314
<212> DNA
<213> Zea mays

<400> 219

cctgagcagc gagtccccga ttttatcaag gcaggtgctg atattgttag tgtccactgt 60

gaacagacat cgaccatcca tttgcaccga acagtcaatc agattaaaag tctaggagca 120

aaggcaggag ttgttttgaa tccagcgact ccactcactg caattgatta tgttcttgat 180

gttgttgacc tggtgctgat tatgtctgtg aatcctgggt ttggtggcca gagctttatc 240

gagagtcaag taaagaaaat tgcagaactg agagagttat gtgcagagaa gggagtgaac 300

ccctggattg aggt 314

<210> 220
<211> 305
<212> DNA
<213> Zea mays

<400> 220

ggcaggtgct gatattgtta gtgtccactg tgaacagaca tcgaccatcc atttgcaccg 60

aacagtcaat cagattaaaa gtctaggagc aaaggcagga gttgtttgaa tccagcgact 120

ccactcactg caattgatta tgttcttgat gttgttgacc tggtgctgat tatgtctgtg 180

aatcctgggt ttggtggcca gagctttatc gagagtcaag taaagaaaat tgcagaactg 240

agaaggttat gtgcagagaa gggagtgaac ccctggattg aggttgatgg tggtgttggt 300

ccgaa 305

<210> 221
<211> 280
<212> DNA
<213> Zea mays

<400> 221

atccatttgc accgaacagt caatcagatt aaaagtctag gagcaaaggc aggagttgtt 60

ttgaatccag cgactccact cactgcaatt gattatgttc ttgatgttgt tgacctggtg 120

ctgattatgt ctgtgaatcc tgggtttggt ggccagagct ttatcgagag tcaagtaaag 180

aaaattgcag aactgagaag gttatgtgca gagaagggag tgaacccctg gattgaggtt 240

gatggtggtg ttggtccgaa aaatgcctac aaggttattg 280

<210> 222
<211> 284
<212> DNA
<213> Zea mays

<400> 222

ctgtctgcaa actttgcgaa cgttggtgat caggtaaaag ctgtggaggt ggcaggatgc 60

gactggattc atgtcgatgt catggacggg cgctttgtgc caaacatcac aattggaccc 120

ttggttgttg atgctctgcg tccagtgact gatcttccgt tggatgtaca tctgatgatt 180

gtggaacctg agcagcgagt ccccgatttt atcaaggcag gtgctgatat tgttagtgtc 240

cactgtgaac agacatcgac catccatttg caccgaacag tcaa 284

<210> 223
<211> 218
<212> DNA
<213> Zea mays

<400> 223

tgttagtgtc cactgtgaac agacatcgac catccatttg caccgaacag tcaatcagat 60

taaaagtcta ggagcaaagg caggagttgt tttgaatcca gcgactccac tcactgcaat 120

tgattaggtt cttgatgtgg ttgacctggt gctgattatg tctgtgaatc ctgggtttgg 180

tggccagagc tttatcgaga gtcaggtaaa gaaaattg 218

<210> 224
<211> 249
<212> DNA
<213> Zea mays

<400> 224

tatcaaggca ggtgctgata ttgttagtgt ccactgtgaa cagacatcga ccatccattt 60

gcaccgaaca gtcaatcaga ttaaaagtct aggagcaaag gcaggagttg ttttgaatcc 120

agcgactcca ctcactgcaa ttgattatgt tcttgatgtt gtcgccctgg tgctgattat 180

gtctgtaaat cctgggtttg gtggccagag ctttatcgag agtcaagtaa agaaaattgc 240

agaactgag 249

<210> 225
<211> 316
<212> DNA
<213> Zea mays

<400> 225

gataaggtgc gcacactgag aaagaagtac ccttcccttg acatagaggt tgatggtggt 60

ctaggtcctt caaccataga cgtggccgca tctgctgggg ccaattgcat cgtcgctgga 120

agctctatat ttggcgctgc ggacccagga gccatcatat ctgtgctgag gaagagcgtc 180

gagggctctc agaacaaaaa ctgattttgg tgtttctgct gtaaagtact ccctccgttt 240

ttttttattc gtcgcgtttt agttcaaaca tgaactagcg gacgactgat attcgagaat 300

ggagggagta cttcga 316

<210> 226
<211> 301
<212> DNA
<213> Zea mays

<400> 226

ggttgatggt ggtctaggtc cttcaaccat agacgtggcc gcatctgctg gggccaattg 60

catcgtcgct ggaagctcta tatttggcgc tgcggaccca ggagccatca tatctgtgct 120

gaggaagagc gtcgagggct ctcagaacaa aaactgattt tggtgtttct gctgtaaagt 180

actccctccg tttttttatt cgtcgcgttt tagttcaaac atgaactagc ggacgactga 240

tattcgagaa tggagggatt acttcgaccc tgcacgtcag atgagctgat cctcacattg 300

c 301

<210> 227
<211> 247
<212> DNA
<213> Zea mays

<400> 227

cggttattga agctggcgca aatgccattg tcgcaggttc tgcagttttt gcggtgtcca 60

gactaacact gcagctatca aaggaataca gaccagccaa agacctctag ctgtagccgc 120

ataaggcgct ggacgtgtaa tcatttactc tgtgcaagtt taccagtgat gcgatctgta 180

tagttgtgtg tcttgtccaa ccatacgtat accgagatga aaagagacgg aggcagtgaa 240

gaactat 247

<210> 228
<211> 319
<212> DNA
<213> Zea mays

<400> 228

attgagagag ccagagaggt gggcagatgg cgacaccgtc gtcgtcgctt tgctccagct 60

tcgcctccct gcggaccgcc tccatcggcc acccccgcgg catcgcgtca tctacgccca 120

ggaaggcgtt ccaagtgagg gcatcagctc gggttgacaa gttctcaaag agtgatatca 180

ttgtgtcccc ttcgattctg tctgcaaact tcgccaagct tggtgatcag gtaaaagccg 240

tggaggtggc aggatgtgac tggattcatg tcgatgtcat ggacgggcgc tttgtgccaa 300

atatcacaat tggacctttt 319

<210> 229
<211> 301

<212> DNA
<213> Zea mays

<400> 229

gagagaggcg cgcagatggc gacgccgtcg tcgtcgcttt gctccagctt cgcctccctg 60

cggaccgcct ccatcggcca cccccgtggc atcgcctcct ccacgcccag gaaggcattc 120

catgtgaggg catcagctcg ggttgacaaa ttctcaaaga gtgacatcat cgtgtcccct 180

tcgattctgt ctgcaaactt tgcgaacttg gtgatcaggt aaaagctgtg gaggtggcag 240

gatgcgactg gattcatgtc gatgtcatgg acgggcgctt tgtgccaaac atcacaattg 300

g 301

<210> 230
<211> 268
<212> DNA
<213> Zea mays

<400> 230

cgcagatggc gacgccgtcg tcgtcgcttt gctccagctt cgcctccctg cggaccgcct 60

ccatcggcca cccccgtggc atcgcctcct ccacgcccag gaaggcattc catgtgaggg 120

catcagctcg ggttgacaag ttctcaaaga gtgacatcat cgtgtcccct tcgattctgt 180

ctgcaaactt tgcgaacttc ggtgatcagg taaaagctgt ggaggtggca ggatgcgact 240

ggattcatgt cgatgtcatg gatgggcg 268

<210> 231
<211> 256
<212> DNA
<213> Zea mays

<400> 231

aagcgtcgtc gtcgctttgc tccagcttcg cctccctgcg gaccgcctcc atcggccacc 60

cccgtggcat cgcctcctcc acgcccagga aggcattcca tgtgagggca tcagctcggg 120

ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc gattctgtct gcaaactttg 180

cgaagcttgg tgatcaggta aaagctgtgg aggtggcagg cggcgactgg attcatgtcg 240

atgtcatgga cgggcg 256

<210> 232
<211> 319
<212> DNA
<213> Zea mays

<400> 232

gctcttgcaa caagccaaac aacccagtgg ctgctagccg agacagggga tagattgaga 60

gagaggcgcg cagatggcga cgccgtcgtc gtcgctttgc tccagcttcg cctccctgcg 120

gaccgcctcc atcggccacc cccgtggcat cgcctcctcc acgcccagga aggcattcca 180

tgtgagggca tcagctcggg ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc 240

gattctgtct gcaaactttg cgaactctgg tgatcaggta aaagctgtgg aggtggcagg 300

atgcgactgg attcatgtc 319

<210> 233
<211> 287
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 233

ccagtggctg ctagccgaga cggggataga ttgacagaca ggcgcgcaga tcgcgacgcc 60

gtcgtcgtcg ctttgctcca gcttcgcctc cctgcggacc gcctccatcg gccacccccg 120

tggcatcgcc tcctccacgc ccagtcaagg cattccatgt gagggcatca gctcgggttc 180

acaaattctc aaagagtgac atcatcgtgt ccccttcgat tctgtctgca aactttgcga 240

acttggtgat caggtanaag ctgtggaggt ggcaggatgc gactgga 287

<210> 234
<211> 261
<212> DNA
<213> Zea mays

<400> 234

agaggggata gattgagaga gccagagagg tgggcagatg gcgacaccgt cgtcgtcgct 60

ttgctccagc ttcgcctccc tgcggaccgc ctccatcggc cacccccgcg gcatcgcgtc 120

atctacaccc aggaaggcgt tccaagtgag ggcatcagct cgggttgaca agttctcaaa 180

gagtgatatc attgtgtccc cttcgattct gtctgcaaac ttcgccaagc ttggtgatca 240

ggtaaaagcc gtggaggtgg c 261

<210> 235
<211> 299
<212> DNA
<213> Zea mays

<400> 235

gctcttgcaa caagccaaac aacccagtgg ctgctagccg agacagggga tagattgaga 60

gagaggcgcg cagatggcga cgccgtcgtc gtcgctttgc tccagcttcg cctccctgcg 120

gaccgcctcc atcggccacc cccgtggcat cgcctcctcc acgcccagga aggcattcca 180

tgtgagggca tcagctcggg ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc 240

gattctgtct gcaaactttg cgaacgttgg tgatcaggta aaagctgtgg aggtggcag 299

<210> 236
<211> 241
<212> DNA
<213> Zea mays

<400> 236

attgacagac aggcgcgcag atggcgacgc cgtcgtcgtc gctttgctcc agcttcgcct 60

ccctgcggac cgcctccatc ggccaccccc gtggcatcgc ctcctccacg cccaggaagg 120

cattccatgt gagggcatca gctcgggttg acaaattctc aaagagtgac atcatcgtgt 180

ccccttcgat tctgtctgca aactttgcga agcttggtga tcaggtaaaa gctgtggagg 240

t 241

<210> 237
<211> 293
<212> DNA
<213> Zea mays

<400> 237

ctcttgcaac aagccaaaca acccagtggc tgctagccga gacaggggat agattgagag 60

agaggcgcgc agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc ctccctgcgg 120

accgcctcca tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa ggcattccat 180

gtgagggcat cagctcgggt tgacaaattc tcaaagagtg acatcatcgt gtccccttcg 240

attctgtctg caaactttgc gaactgtggt gatcaggtaa aagctgtgga ggt 293

<210> 238
<211> 325
<212> DNA
<213> Zea mays

<400> 238

accaaatcgc ttaccgcccc cgaagcgtct cggttcgcat agcagagctg ctcttgcaac 60

aagccaaaca acccagtggc tgctagccga gacaggggat agattgagag agaggcgcgc 120

agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc ctccctgcgg accgcctcca 180

tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa ggcattccat gtgagggcat 240

cagctcgggt tgacaaattc tcaaagagtg acatcatcgt gtccccttcg attctgtctg 300

caaactttgc gaacgttggt gatca 325

<210> 239
<211> 301
<212> DNA
<213> Zea mays

<400> 239

cgaagctctc ggttcgcata gcagagctgc tcttgcaaca agccaaacaa cccagtggct 60

gctagccgag acaggggata gattgagaga gaggcgcgca gatggcgacg ccgtcgtcgt 120

cgctttgctc cagcttcgcc tccctgcgga ccgcctccat cggccacccc cgtggcatcg 180

cctcctccac gcccaggaag ggattccatg tgagggcatc agctcgggtt gacaaattct 240

caaagagtga catcatcgtg tccccttcga ttctgtctgc aaactttgcg aagcttggtg 300

a 301

<210> 240
<211> 288
<212> DNA
<213> Zea mays

<400> 240

agcagagctg ctcttgcaac aagccaaaca acccagtggc tgctagccga gacaggggat 60

agattgagag agaggcgcgc agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc 120

ctccctgcgg accgcctcca tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa 180

ggcattccat gtgagggcat cagctcgggt tgacaaattc tcaaagagtg acatcatcgt 240

gtccccttcg attctgtctg caaactttgc gaactgtggt gatcaggt 288

<210> 241
<211> 304
<212> DNA
<213> Zea mays

<400> 241

aatcgcttac cgcccccgaa gcgtctcggt tcgcatagca gagctgctct tgcaacaagc 60

caaacaaccc agtggctgct agccgagaca ggggatagat tgagagagag gcgcgcagat 120

ggcgacgccg tcgtcgtcgc tttgctccag cttcgcctcc ctgcggaccg cctccatcgg 180

ccacccccgt ggcatcgcct cctccacgcc caggaaggca ttccatgtga gggcatcagc 240

tcgggttgac aaattctcaa agagtgacat catcgtgtcc ccttcgattc tgtctgcaaa 300

cttt 304

<210> 242
<211> 229
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 242

cataactact ctgccaccaa tccggggagg aatcaaccta gcggtaagcg gacatggcgg 60

cggcgaagat agcgccgtcg atgctctcgt cggactttgc caacctcgct tcggaggctg 120

agcgcatggt ccgcctaggc gccgactggc tacatatgga catcatggat gggcacttcg 180

ttcctaacct gactattggg gctccggtga tccagangct tgagaaata 229

<210> 243
<211> 269
<212> DNA
<213> Zea mays

<400> 243

gctacatatg gacatcatgg atgggcactt cgttcctaac ctgactattg gggctccggt 60

gatccagagc ttgaggaaac ataccaaagc atatttggac tgccatctta tggtcacaaa 120

gccttcagat tacgtagaac catttggaaa ggctggcgct tctggattca cattccatat 180

agaagttgct agagacaact ggcaagatct catccaaagc attaaatcaa agggtatgcg 240

gcctggtgta tcattgaggc caggtactc 269

<210> 244
<211> 385
<212> DNA
<213> Zea mays

<400> 244

ccgggctcaa ccaacgcgtc aggatgtttt gaaccaacca acccaatcaa cggaaattga 60

taacttcctg gaggtggttg acctgtggcg gataaggtcg gtaaacccgg ggttgggggg 120

caaaacctta accaaaagtc aattaaagaa aattgcaaaa ctgaaaaggt aatgtgcaaa 180

aaagggagtg aaccccggga ttgaggttga tggtggtgtt ggtccgaaaa atgcctacaa 240

ggttattgaa gctggcgcaa atgccattgt cgcaagttct gcagtttttg gggctccaga 300

ctacgctgaa gctatcaaag gaataaagac cagccaaaga cctctagctg tagccgcata 360

aagagctgga cgtgtaatca tttac 385

<210> 245
<211> 389
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 245

gaccaagccg tccaatcaag gtggaggcca tggatgggcc ctttgtgcca aacatcacaa 60

ttggaccctg ggtgttgat gctctgcgtc cagtgactga tcttccgttg gatgtacatc 120

tgatgattgt ggaacctgag cagcgagtcc ctgattttat caaggcaggt gctgatattg 180

ctagtgtcca ctgtgaacag acatcgacct tcatttgcac cgaacagtca atcagattaa 240

aagtctagga gcanaggcag ggattgttnt gaatccagcg actccactca ctgcaattga 300

ttacgttctt gatgttgttg acctggtgct gattatgtct gtgaatcctg ggtttgttgg 360

cagagcttta tcgagagtca agtaaggaa 389

<210> 246

<211> 412
<212> DNA
<213> Zea mays

<400> 246

gtgtcccctt cgattctgtc tgcaaacttt gcgaagcttg gtgatcaggt aaaagctgtg 60

gaggtggcag gatgcgactg gattcatgtc gatgtcatgg acgggcgctt tgtgccaaac 120

atcacaattg gacccttggt tgttgatgct ctgcgtccag tgactgatct tccgttggat 180

gtacatctga tgattgtgga acctgagcag cgagtccccg attttatcaa ggcaggtgct 240

gatattgtta gtgtccactg tgaacagaca tcgaccatcc atttgcaccg aacagtcaat 300

cagattaaaa gtctaggagc aaaggcagga gttgttttga atccagcgac tccactcact 360

gcaattgatt acgttcttga tgttgttgac ctggtgctga ttatgtctgt ga 412

<210> 247
<211> 397
<212> DNA
<213> Zea mays

<400> 247

gatgctctgc gtccagtgac tgatcttccg ttggatgtac atctgatgat tgtggaacct 60

gagcagcgag tccctgattt tatcaaggca ggtgctgata ttgttagtgt ccactgtgaa 120

cagacatcga ccatccattt gcaccgaaca gtcaatcaga ttaaaagtct aggagcaaag 180

gcaggagttg ttttgaatcc agcgactcca ctcactgcaa ttgattacgt tcttgatgtt 240

gttgacctgg tgctgattat gtctgtgaat cctgggtttg gtggccagag ctttatcgag 300

agtcaagtaa agaaaattgc agaactgaga aggttatgtg cagagaaggg agtgaacccc 360

tggattgagg ttgatggtgg tgttggtccg aaaaatg 397

<210> 248
<211> 403
<212> DNA
<213> Zea mays

<400> 248

ggaggtggca ggatgcgact ggattcatgt cgatgtcatg gacgggcgct ttgtgccaaa 60

catcacaatt ggacccttgg ttgttgatgc tctgcgtcca gtgactgatc ttccgttgga 120

tgtacatctg atgattgtgg aacctgagca gcgagtcccc gattttatca aggcaggtgc 180

tgatattgtt agtgtccact gtgaacagac atcgaccatc catttgcacc gaacagtcaa 240

tcagattaaa agtctaagag caaaggcagg gaattgtttg aatccagcga cttcacttac 300

tggaattgat tatggtcctg atggtggtga cctggtgctg attatgtctg tgaatcctgg 360

gtttggtggc caaagcttta ttgagagtca agttaaggaa att 403

<210> 249
<211> 419
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 249

gtgaaagccg tggaggtggc aggatgttac tggattcatg tcgatgtcat ggacgggcgc 60

tttgtgccaa atatcacaat tggacctttg gttgttgatg ctctgcgtcc tgtgactgat 120

cttccattgg atgtacatct gatgattgtg gaacctgagc agcgagtccc tgattttatc 180

aaggcaggtg ctgatattgt tagtgtccac tgtgaacaaa catcgaccat ccatttgcac 240

agaacagtca atcagattaa aagtctagga gcaaaagcag gagttgtttt gaatccagcg 300

actccactca atgcaattga ttacattctt gatgttgttg acctggtgtt gattatgtct 360

gtgaatcctg ggtttggtgg ccagagcttt atcgagagtc aagtnaggaa aattgcaga 419

<210> 250
<211> 451
<212> DNA
<213> Zea mays

<400> 250

cgatgtcatg gacgggcgct ttgtgccaaa catcacaatt ggacccttgg ttgttgatgc 60

tctgcgtcca gtgactgatc ttccgttgga tgtacatctg atgattgtgg aacctgagca 120

gcgagtcccc gattttatca aggcaggtgc tgatattgtt agtgtccact gtgaacagac 180

atcgaccatc catttgcacc gaacagtcaa tcagattaaa agtctaggag caaaggcagg 240

agttgttttg aatccagcga ctccactcac tgcaattgat tatgttcttg atgttgttga 300

cctggtgctg attatgtctg tgaatcctgg gtttggtggc cagagcttta tcgagagtca 360

agtaaagaag attgcagaac tgagaaggtt atgtgcagag aagggagtga acccctggat 420

tgaggttgat ggtggtgttg gtcccaaaaa t 451

<210> 251
<211> 389
<212> DNA
<213> Zea mays

<400> 251

cttggtgatc aggtaaaagc tgtggaggtg gcatgatgcg actggattca tgttgatgtc 60

atggatgggc gctttgtggc aaacatcaca attggaccct tggttgttga tgctctgcgt 120

ccagtgactg atcttccgtt ggatgtacat ctgatgattg tggaacctga gcagcgagtc 180

cctgatttta tcaaggcagg tgctgatatt gatagtgtcc actgtgaaca gacatcgacc 240

attcatttgc accgaacagt caatcagatt aaaagtctat gagcaaaggc aggagttgtt 300

gtgaatccag cgactgcact cactgcaatt gattacgttc ttgatgatga tgacctggtg 360

ctgattatgt ctgtgaatcc tgggtttgg 389

<210> 252
<211> 426
<212> DNA
<213> Zea mays

<400> 252

ctatgaacag acatcgacca tccatttgca ccgaacaatc aatcagatta aaagtctagg 60

agcaaaggca ggagttgttt tgaatccagc gactccactc actgcaattg attaggggct 120

tgatgttgtt gacctggtgc tgattagggg ggtgaatcct gcgtttggtg gccagagctt 180

tatcgagagt caagtaaaga aaattgcaga actgagaagg ttatgtgcag agaagggagt 240

gaacccctgg attgaggttg atggtggtgt tggtccgaaa aatgcctaca aggttattga 300

agctggcgca aattctattt tctcaggttc tgcagttttt ggggctccag actacgctga 360

agctatcaaa tggaataaga ccatccaaag acctctagct gtagccgcat aaacaacttg 420

acgtgt 426

<210> 253
<211> 380
<212> DNA
<213> Zea mays

<400> 253

cggacgcgtg ggcggacgcg tgggctgaga aggttatgtg cagagaaggg agtgaacccc 60

tggattgagg ttgatggtgg tgttggtccg aaaaatgcct acaaggttat tgaagctggc 120

gcaaatgcca ttgtcgcagg ttctgcagtt tttggggctc cagactacgc tgaagctatc 180

aaaggaataa agaccagcca aagacctcta gctgtagccg cataaggagc tggacgtgta 240

atcatttact ctgtgcaagt ttaccagtga tgcgatctgt atagatgtgt gtcttgtcca 300

gccatacgta taccggagat gaaaagagac ggaagcagtg aagaaatatc cttttttttt 360

cttctcattt ttcacgaaga 380

<210> 254
<211> 375
<212> DNA
<213> Zea mays

<400> 254

agagagccag agaggtgggc agatggcgac accgtcgtcg tcgctttgct ccagcttcgc 60

ctccctgcgg accgcctcca tcggccaccc ccgcggcatc gcgtcatcta cgcccaggaa 120

ggcgttccaa gtgagggcat cagctcgggt tgacaagttc tcaaagagtg atatcattgt 180

gtccccttcg attctgtctg caaacttcgc caagcttggt gatcaggtaa aagccgtgga 240

ggtggcagga tgtgactgga ttcatgtcga tgtcatggac gggcgctttg tgccaaatat 300

cacaattgga cctttggttg ttgatgctct gcgtcctgtg actgatcttc cattggatgt 360

acatctgatg attgt 375

<210> 255
<211> 429
<212> DNA
<213> Zea mays

<400> 255

cacacgcgtc cgcaacaagc caaacaaccc agtggctgct agccgagaca ggggatagat 60

tgagagagag gcgcgcagat ggcgacgccg tcgtcgtcgc tttgctccag cttcgcctcc 120

ctgcggaccg cctccatcgg ccaccccgt ggcatcgcct cctccacgcc caggaaggca 180

ttccatgtga gggcatcagc tcgggttgac aaattctcaa agagtgacat catcgtgtcc 240

ccttcgattc tgtctgcaaa ctttgcgaag cttggtgatc aggtaaaagc tgtggaggtg 300

gcaggatgcg actggattca tgtcgatgtc atggacgggc gctttgtgcc aaacatcaca 360

attggaccct tggttgttga tgctctgcgt ccagtgactg atcttccgtt ggatgtacat 420

ctgatgatg 429

<210> 256
<211> 424
<212> DNA
<213> Zea mays

<400> 256

atcgcttacc gcccccgaag cgtctcggtt cgcatagcag agctgctctt gcaacaagcc 60

aaacaaccca gtggctgcta gccgagacag gggatagatt gagagagagg cgcgcagatg 120

gcgacgccgt cgtcgtcgct ttgctccagc ttcgcctccc tgcggaccgc ctccatcggc 180

cacccccgtg gcatcgcctc ctccacgccc aggaaggcat tccatgtgag ggcatcagct 240

cgggttgaca aattctcaaa gagtgacatc atcgtgtccc cttcgattct gtctgcaaac 300

tttgcgaagc ttggtgatca ggtaaaagct gtggaggtgg caggatgcga ctggattcat 360

gtcgatgtca tggacgggcg ctttgtgcca aacatcacaa ttggaccctt ggttgttgat 420

gctc 424

<210> 257
<211> 419
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 257

cgcccccgaa gcgtctcggt tcgcatagca aagctgctct tgcaacaagc caaacaaggc 60

antggctgct agccgagaca ggggatagat tgagagagag gcgcgcagat ggcgacgccg 120

tcgtcgtcgc tttgctccag cttcgcctcc ctgcggaccg cctccatcgg ccacccccgt 180

ggcatcgcct cctccacgct caggaaggca ttccatgtga gggcatcagc tcgggttgac 240

aagttctcaa agagtgacat catcgtgtcc ccttcgattc tgtctgcaaa ctttgcgaag 300

cttggtgatc aggtaaaagc tgtggaggtg gcaggatgcg actggattca tgtcgatgtc 360

atggacgggc gctttgtgcc aaacatcaca attggaccct tggtttgtga tgctctgcg 419

<210> 258
<211> 416
<212> DNA
<213> Zea mays

<400> 258

agaaccaaat cgcttaccgc ccccgaagcg tctcggttcg catagcaaag ctgctcttgc 60

aacaagccaa acaacccagt ggctgctagc cgagacaggg gatagattga gagagaggcg 120

cgcagatggc gacgccgtcg tcgtcgcttt gctccagctt cgcctccctg cggaccgcct 180

ccatcggcca cccccgtggc atcgcctcct ccacgctcag gaaggcattc catgtgaggg 240

catcagctcg ggttgacaag ttctcaaaga gtgacatcat cgtgtcccct tcgattctgt 300

ctgcaaactt tgcgaagctt ggtgatcagg taaaagctgt ggaggtggca ggatgcgact 360

ggattcatgt cgatgtcatg gacgggcgct ttgtgccaaa catcacaatt ggaccc 416

<210> 259
<211> 390
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 259

caacaagcca aacaacccag tggctgctag ccgagacagg ggatagattg agagagaggc 60

gcgcagatgg cgacgccgtc gtcgtcgctt tgctccagct tcgcctccct gcggaccgcc 120

tccatcggcc acccccgtgg catcgcctcc tccacgccca ggaaggcatt ccatgtgagg 180

gcatcagctc gggttgacaa attctcaaag agtgacatca tcgtgtcccc ttcgattctg 240

tctgcaaact ttgcgaagct tggtgatcag gtaaaagctg tggaagtggc aggatgcgac 300

tggattcatg tcgatgtcat ggacgggcgc tttgtgccaa acatcacaat tggacccttg 360

ngttgtgatg ctctgcgtcc agtgactgat 390

<210> 260
<211> 415
<212> DNA
<213> Zea mays

<400> 260

gttttgtttg ttgtccgcct ggcgcctggc cccataacta ctctgccaca atccggggaa 60

gaatcaacct agcggtaagc ggacatggcg gcggcgaaga tagcgccgtc gatgctctcg 120

tcggactttg ccaacctcgc ttcggaggct gagcgcatgg tccgcctagg cgccgactgg 180

ctacatatgg acatcatgga tgggcacttc gttcctaacc tgactattgg ggctccggtg 240

atccagagct tgaggaaaca taccaaagca tatttggact gccatcttat ggtcacaaag 300

ccttcagatt acgtagaacc atttggaaag gctggcgctt ctggattcac attccatata 360

gaagttgcta gagacaactg gcaagatctc atccaaagca ttaaatcaaa gggta 415

<210> 261
<211> 257
<212> DNA
<213> Glycine max

<400> 261

aaaatttcaa ccacagtgaa ggctacatct cgtgttgaca agttttcaaa aagcgatatc 60

attgtctctc catccattct ttctgcaaac tttgcaagat tgggacaaca ggtgaaagca 120

ctgcagttgg ctggttgtga ttggcttcac gttgatgtaa tggatggccg ttttgttcca 180

aatattacaa ttggacctct tgtcggctga tgcattgcgc cctgtgacag atcttccttt 240

ggatgtacac ctgatga 257

<210> 262
<211> 272
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 262

gggagttgaa aganagaaag gaaggatggg agtgacaccg aaaattgctc cttcgatgct 60

ctcttccgac ttcgccaatt tggcttccga ggctcagcgc atgctccact tcggcgccga 120

ttggctccac atggacatca tggatgggca ttttgtcccc aatttaacta ttggcgctcc 180

agttattgaa agtttgagaa agcacacaaa gggatatttg gattgtcacc ttatggttac 240

aaatcctctt gattatgttg agnccttggc aa 272

<210> 263

<211> 260
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 263

agttgaaaga nagaaaggaa ggatgggagt gacaccgaaa attgctcctt cgatgctctc 60

ttccgacttc gccaatttgg cttccgaggc tcagcgcatg ctccacttcg gcgccgattg 120

gctccacatg gacatcatgg atgggcattt tgtccccaat ttaactattg gcgctccagt 180

tattgaaagt ttgagaaagc acacaaaggg atatttggat tgtcacctta tggttacaaa 240

tcctcttgat tatgttgagc 260

<210> 264
<211> 266
<212> DNA
<213> Glycine max

<400> 264

caaggaagga tgggagtgac accgaaaatt gctccttcga tgctctcttc cgacttcgcc 60

aatttggctt ccgaggctca gcgcatgctc cacttcggcg ccgattggct ccacatggac 120

atcatggatg ggtcttttgt ccccaattta actattggcg ctccagttat tgaaagtttg 180

agaaagcaca caaagggata tttggattgt caccttatgg ttacaaatcc tcttgattat 240

gttgagccct tggcaaaagc tggtgc 266

<210> 265
<211> 228
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 265

tgacaccgaa aattgctcct tcgatgctcn cttccgantt cgcnaatttg gcttccgagg 60

ctcagcgcat gctccacttc ggcgccgatt ggctccacat ggacatcatg gntgggnatt 120

ttgtccccaa tttaactatt ggcgctccag ttattganag tttgagaaag cacacaaagg 180

gatatttnng attgtcacct tatggttaca aatcctcttg attatgtt 228

<210> 266

<211> 243
<212> DNA
<213> Glycine max

<400> 266

caaccataga tgtggccgca tcagcagggg caaactgcat tgttgctgga agttcagtgt 60

ttggtgcccc tgagccagtt caagtaatat ccttactaag gaattctgtt gagaaagccc 120

agcaaacctt gatacagtaa aaaaaaaatg tcgttttaag ttgcagtaca cttcacaact 180

ttgcataaac aatatgctta atgtttaaca ttttccataa gttgaataaa agatcatgtg 240

act 243

<210> 267
<211> 266
<212> DNA
<213> Glycine max

<400> 267

agaggttgat ggtggtttag ggccttcaac catagacgtg gccgcatcag caggggcaaa 60

ttgcattgtt gctggaagtt ctgtttttgg tgcacctgag ccagctcaag taatatccta 120

ctgaggagtt ctgttgagaa agcccagcaa acctcgatac agtaaaacaa tgtcgtttta 180

agttgcagta tacttcacaa ctttacataa acaatatgct aatgttaaca tttcataagt 240

tgaataaaag atcaagtgct tgaaaa 266

<210> 268
<211> 229
<212> DNA
<213> Glycine max

<400> 268

gaaaatttct gacttgagaa gagtgtgcgc ggaaaaggga gtgaatccat ggattgaagt 60

agatggtgga gttggtccag caaatgctta caaggtgatt gaggctggag ccaatgctct 120

ggttgcaggc tctgcttgtt tggagctaaa gattatgccg aagctataag aggaatcaaa 180

accagcaaaa gacctgaagc agttgctgtg tgaaatgccc atgtggttc 229

<210> 269
<211> 266
<212> DNA

<213> Glycine max

<400> 269

cccccatccc caccccaact tgtatattgt gcataatatc tatctgcatt ctctctcttc 60

agggagtgaa tccatggatt gaagtagatg gtggagttgg tccagcaaat gcttacaagg 120

tgattgaggc tggagccaat gctctggttg caggctctgc tgtgtttgga gctaaagatt 180

atgccgaagc tataagagga atcaaaacca gcaaaagacc tgaagcagtt gctgtgtgaa 240

atgcccatgt ggttcaatat tcaccg 266

<210> 270
<211> 257
<212> DNA
<213> Glycine max

<400> 270

agcgatatca ttgtctctcc gtccattctt tctgcaaact tttcaaaatt gggagagcag 60

gtgaaagcag tggaattggc tggttgtgat tggattcacg ttgatgtaat ggatggtcgc 120

tttgttccaa atattacaat tggacctctt gtggttgatg cattgcgccc tgtgacagat 180

cttcctttgg atgtacacct gatgattgta gacctgaaca aagggtacca gattttatta 240

aggcaggagc tgatata 257

<210> 271
<211> 274
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 271

caagttttca aaaagcgata tcattgtttc tccatccatt ctttctgcaa actttgcaaa 60

attggganag cangtgaaag cagtggagtn gnnggntggt aatnggntca angtngatgt 120

aatggatggc cngtttngtn ccaaatatta caattggacc tcttgtggtt gatgcattgc 180

cgcccctgtg acagatcttc cttnggatgt acacctgatg attgtagacc ctgaacaaag 240

ggtaccagat tttattaagg caggagcccg atac 274

<210> 272
<211> 281

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 272

cttcttcctt gtgttcatcg accctccaat cccaaatcaa tggattctgc cttcacaaaa 60

cctctctttc ccatcctcgt tccctcactt tctccaggaa gaaaatttca accacagtga 120

aggctacatc tcgtgttgac aagttttcaa aaagcgatat cattgtttct ccatccattc 180

tttctgcaaa ctttgcaaaa ttgggagagc aggtgaaagc agtggagttg gctggttntg 240

atggattcac gttgatgtaa tggatgggcg tttgttccaa a 281

<210> 273
<211> 256
<212> DNA
<213> Glycine max

<400> 273

gatggctgca acctcttcct tgtgctcatc gaccctccaa tcccagatca atggattctt 60

ccttcacaaa acctctcttt cccatactcc ttccctcact ttctccagga ggaaaatttc 120

aaccacagtg aaggctacat ctcgagtcga caagttttca aaaagcgata tcattgtctc 180

tccgtccatt ctttctgcaa acttttcaaa attggagagc aagtgaaagc agtagaattg 240

gctggttgtg attgga 256

<210> 274
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 274

gattgctgag tcaaacttga attgaaggtg aagaaggaga tggcagnaac ttcttccttg 60

tgttnatcga ncctncaatc ccaaatcaat ggattctgcn ttcacaaaac ctctntttcc 120

catcctcgtt ccctnacttt ctcnaggaag aaaatttcaa ccacagtgaa ggctacatct 180

cgtgttnaca agttttcaaa aagcgatatc attgtttctc catccattct ttntgcaaac 240

tttgcaaaat tgggagagca ggtgaaagca gtg 273

<210> 275
<211> 260
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 275

ggtnangtaa acttganttg aagtgaagaa ggagatggct gcaacctctt ccttgtgctt 60

catcgaccct ccaatcccag atcaatggat tcttccttca caaaacctct ctttcccata 120

ctccttccct cactttctcc aggaggaaaa tttcaaccac agtgaaggct acatctcgag 180

tcgacaagtt ttcaaaaagc gatatcattg tctctccgtc cattctttct gcaaactttt 240

caaaattggg agagcaggtg 260

<210> 276
<211> 247
<212> DNA
<213> Glycine max

<400> 276

gtcaaacttg aattgaaggt gaagaaggag atggcagcaa cttcttcctt gtgttcatcg 60

accctccaat cccaaatcaa tggattctgc cttcacaaaa cctctctttc ccatcctcgt 120

tccctcactt tctccaggaa gaaaatttca accacagtga aggctacatc tcgtgttgac 180

aagttttcaa aaagcgatat cattgtttct ccatccattc tttctgcaaa ctttgcaaaa 240

ttgggag 247

<210> 277
<211> 255
<212> DNA
<213> Glycine max

<400> 277

ggattggtga ggtaaacttg aattgaagtg aagaaggaga tggctgcaac ctcttccttg 60

tgctcatcga ccctccaatc ccagatcaat ggattcttcc ttcacaaaac ctctctttcc 120

catactcctt ccctcacttt ctccaggagg aaaatttcaa ccacagtgaa ggctacatct 180

cgagtcgaca agttttcaaa aagcgatatc attgtctctc cgtccattct ttctgcaaac 240

ttttcaaaat tggga 255

<210> 278
<211> 254
<212> DNA
<213> Glycine max

<400> 278

cgattggtga ggtaaacttg aattgaagtg aagaaggaga tggctgcaac ctcttccttg 60

tgctcatcga ccctccaatc ccagatcaat ggattcttcc ttcacaaaac ctctctttcc 120

catacttctt ccctcacttt ctccaggagg aaaatttcaa ccacagtgaa ggctacatct 180

cgagtcgaca agttttcaaa aagcgatatc attgtctctc cgtccattct ttctgcaaac 240

ttttcaaaat tggg 254

<210> 279
<211> 276
<212> DNA
<213> Glycine max

<400> 279

gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct gcaacctctt 60

ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttccttcac aaaacctctc 120

tttcccatac tccttccctc actttctcca ggaggaattt caaccacagt gaaggctaca 180

tctcgagtcg acaagttttc aaaaagcgat atcattgtct ctccgtccat tctttctgca 240

aacttttcaa aattgggaga gcaggtgaaa gcagtg 276

<210> 280
<211> 244
<212> DNA
<213> Glycine max

<400> 280

taggattggt gaggtaaact tgaattgaag tgaagaagga gatggctgca acctcttcct 60

tgtgctcatc gaccctccaa tcccagatca atggattctt ccttcacaaa acctctcttt 120

cccatactcc ttccctcact ttctccagga ggaaaatttc aaccacagtg aaggctacat 180

ctcgagtcga caagttttca aaaagcgata tcattgtctc tccgtccatt ctttctgcaa 240

actt 244

<210> 281
<211> 249
<212> DNA
<213> Glycine max

<400> 281

cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaaggtgaag aaggagatgg 60

cagcaacttc ttccttgtgt tcatcgaccc tccaatccca aatcaatgga ttctgccttc 120

acaaaacctc tctttcccat cctcgttccc tcactttctc caggaagaaa atttcaacca 180

cagtgaaggc tacatctcgt gttgacaagt tttcaaaaag cgatatcatt gtttctccat 240

ccattcttt 249

<210> 282
<211> 262
<212> DNA
<213> Glycine max

<400> 282

cacacacttt tttcaaggca taggattggt gaggcaaact tgaattgaag tgaagaagga 60

gatggctgca acctcttcct tgtgctcatc gaccctccaa tcccagatca atggattctt 120

ccttcacaaa acctctcttt cccatactcc ttccctcact ttctccagga ggaaaatttc 180

aaccacagtg aaggctacat ctcgagtcga caagttttca aaaagcgata tcattgtctc 240

tccgtccatt ctttctgcaa at 262

<210> 283
<211> 249
<212> DNA
<213> Glycine max

<400> 283

ttttgtcaag gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct 60

gcaacctctt ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttccttcac 120

aaaaccttct ttcccatact ccttccctca ctttctccag gaggaaaatt tcaaccacag 180

tgaaggctac atctcgagtc gacaagtttt caaaaagcga tatcattgtc tctccgtcca 240

ttctttctg 249

<210> 284
<211> 265
<212> DNA
<213> Glycine max

<400> 284

cacacagtca cacttttgtg aaggcctagg attgctgagt caaacttgaa ttgaaggtga 60

cgaaggagat ggcagcaact tcttccttgt gttcatcgac cctccaatcc caaatcaatg 120

gattctgcct tcacaaaacc tctctttccc atcctcgttc cctcactttc tccaggaaga 180

aaatttcaac cacagtgaag gctacatctc gtgttgacaa gttttcaaaa agcgatatca 240

ttgtttctcc atccattctt tctgc 265

<210> 285
<211> 250
<212> DNA
<213> Glycine max

<400> 285

caaggcatag gatcggtgag gcaaacttga attgaagtga agaaggagat ggctgcaacc 60

tcttccttgt gctcatcgac cctccaatcc cagatcaatg gattcttcct tcacatcacc 120

tctcttcccc atactccttc cctcactttc tccaggagga aaatttcaac cacagtgaag 180

gctacatctc gagtcgacaa gttttcaaaa gcgatatcat tgtctctccg tccattcttt 240

ctgcaaattt 250

<210> 286
<211> 251
<212> DNA
<213> Glycine max

<400> 286

cacacttttg tcaaggcata ggattggtga ggtaaacttg aattgaagtg aagaaggaga 60

tggctgcaac ctcttccttg tgctcatcga ccctccaatc ccagatcaat ggattcttcc 120

ttcacaaaac ctctctttcc catactcctt ccctcacttt ctccaggagg aaaatttcaa 180

ccacagtgaa ggctacatct cgagtcgaca agttttcaaa agcgatatca ttgtctctcc 240

gtccattctt t 251

<210> 287
<211> 273
<212> DNA
<213> Glycine max

<400> 287

cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaagagtgaa gaaggagatg 60

gcagcaactt cttccttgtg ttcatcgacc ctccaatccc aaatcaatgg attctgcctt 120

cacaaaacct ctctttccca tcctcgttcc ctcactttct ccaggaagaa aatttcaacc 180

acagtgaagg ctacatctcg tgttgacaag ttttcaaaaa gcgatatcat tgtttctcca 240

tccattcttt ctgcaaactt tgcaaaattg ggg 273

<210> 288
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 288

cacacacagt canactttng tgaaggccta ggattggtga gtcaaacttg aattgaaggt 60

gaagaaggag atggcagcaa cttcttcctt gtgttcatcg accctccaat cccaaatcaa 120

tggattctgc cttcacaaaa cctctctttc ccatcctcgt tccctcactt tctccaggaa 180

gaaaatttca accacagtga aggctacatc tcgtgttgac aagttttcaa aaagcggata 240

tcattgtttc tccatccatc tttctgcaaa ttt 273

<210> 289
<211> 259
<212> DNA
<213> Glycine max

<400> 289

cacagtcaca cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaaggtgaag 60

aaggagatgg cagcaacttc ttccttgtgt tcatcgaccc tccaatccca aatcaatgga 120

ttctgccttc acaaaacctc tctttcccat cctcgttccc tcactttctc caggaagaaa 180

atttcaacca cagtgaaggc tacatctcgt gttgacaagt tttcaaaaag cgatatcatt 240

gtttctccat ccattcttt 259

<210> 290
<211> 246
<212> DNA
<213> Glycine max

<400> 290

tttcctcaag gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct 60

gcaacctctt ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttgcttcac 120

aaaacctctc ttgctcatac tccttccctc actttctcca ggcggaaaat ttcaaccaca 180

gtgaaggcta catctcgagt cgacaagttt tcaaaaagcg atatcatgtg gtcgctccgt 240

ccattc 246

<210> 291
<211> 262
<212> DNA
<213> Glycine max

<400> 291

gctggagttg tcttaaaccc cggtaccccc ttaagtgcaa tagaatatat ccttgatgtg 60

gttgatttgg tcttaattat gtccgtaaac cctggctttg gtggccagag ttttattgag 120

agtcaagtaa agaaaatttc tgatttgaga agattgtgtg cggagaaggg agtgaatcca 180

tggattgaag tagatggtgg agttggtcca gcaaatgcat acaaggtgat tgaggctgga 240

gccaatgcac tggttgctgg ct 262

<210> 292
<211> 282
<212> DNA
<213> Glycine max

<400> 292

agggtaccag attttattaa ggcaggagct gatatagtca gtgttcattg tgaacaatct 60

tccaccatcc atttgcatcg tactgttaat caagtgaaaa gtctgggagc taaagctgga 120

gttgtcttaa accctgctac ccccttaagt gcaatagaat atgtcctgat gtggtggatt 180

tggtcttaat tatgtccgta aaccctggct ttggtggcca gagttttatt gagagtcaag 240

taaagaaaat ttctgacttg agaagagtgt gcgcggaaaa gg 282

<210> 293
<211> 249
<212> DNA
<213> Glycine max

<400> 293

gtcgctttgt tccaaatatt acaattggac ctcttgtggt tgatgcattg cgccctgtga 60

cagatcttcc tttggatgta cacctgatga ttgtagagcc tgaacaaagg gtaccagatt 120

ttattaaggc aggagctgat atagtcagtg ttcattgtga acaatcttcc accatccatt 180

tgcatcgtac agttaatcaa gtgaaaagtc tgggagctaa agctggagtt gtcttaaacc 240

ccggtaccc 249

<210> 294
<211> 264
<212> DNA
<213> Glycine max

<400> 294

ggtgaaagca gtagaattgg ctggttgtga ttggattcac gttgatgtaa tggatggtcg 60

ctttgttcca aatattacaa ttggacctct tgtggttgat gcattgcgcc ctgtgacaga 120

tcttcctttg gatgtacacc tgatgattgt agagcctgaa caaagggtac cagattttat 180

taaggcagga gctgatatag tcagtgttca ttgtgaacaa tcttccacca tccatttgca 240

tcgtacagtt aatcaagtga aaag 264

<210> 295
<211> 267
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 295

gtcagtgttc attgtgaaca atcttccncc atccatttgc atcctacagt taacncaagt 60

gaaaagtctg ggagctaaag ctggagttgt cttaaacccc ggtacccccct taagtgcaat 120

agaatatatc cttgatgtgg ttgatttggt cttaattatg tccgtaaacc ctggctttgg 180

tggccagagt tttattgaga gtcaagtaaa gaaaatttct gatttgagaa gattgtgtgc 240

ggagaaggga gtgaatccat ggattga 267

<210> 296
<211> 277
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 296

gtccaattgt aatatttgga acaaaacggc catccattac aattngacct cttgtggttg 60

atgcattgcg ccctgtgaca nctcttcctt tggatgtaca cctgatgatt gtacagcctg 120

aacaaagggt accagatttt attaaggcag gagctgatat agtcagtgtt cattgtgaac 180

aatcttccac catccatttg catcgtactg ttaatcaagt gaaaagtctg ggagctaaag 240

ctggagttgt ctaaaccctg ctaccccctt aagtgca 277

<210> 297
<211> 263
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 297

ggctggagtt gtcttaaacc ccggtacccc cttaagtgca atagaatata tccttgatgt 60

ggttnatttg gtcttaattn tgtaccgtaa accctggctt tggtggccag agttttattg 120

agagtcaagt aaagaaattt ctgatttgag aagattgtgt gcggagaagg gagtgaatcc 180

atggattgaa gtagatggtg ggngttggtc cagcaaatgc atacaggtga tnggaggctg 240

gnagccaaac cntggtgcag gcc 263

<210> 298
<211> 388
<212> DNA
<213> Glycine max

<400> 298

ggagaaagaa agaaaagatg ggaatgacac cgaaaatagc tccttcgatg ctctcttccg 60

acttcgccaa tttggcttcc gaggctcagc gcatgctcca cttcggcgcc gattggctcc 120

acatggacat catggatggg cattttgtcc ccaatttaac tattggcgct ccagttattg 180

aaagtttgag aaagcacaca aaggcatatt tggattgtca ccttatggtt acaaatcctc 240

ttgattatgt tgaacccttg gcaaaagctg gtgcttctgg ttttacattt cacgtagaga 300

catcaaaaga taactggaaa gaacttatcc aaagaatcaa gtcacatggc atgattcctg 360

gtgtagcatt aaagcctggg accccccgt 388

<210> 299
<211> 368
<212> DNA
<213> Glycine max

<400> 299

gatggccgtt ttgttccaaa tattacaatt ggacctcttg tggttgatgc attgcgccct 60

gtgacagatc ttcctttgga tgtacacctg atgattgtac agcctgaaca aagggtacca 120

gattttagta aggcacgagc tgatatagtc agtgttcatt gtgaacaatc ttccaccatc 180

catttgcatc gtactgttaa tcaagtgaaa agtctgggag ctaaagctgg agttgtctta 240

aaccctgcta ccccccttaag tgcaatagaa tatgtccttg atgtggtgga tttggtccta 300

attaagtccg taaaccctgg ctttggtggc cacagtttta atgagagtca agtaaagaaa 360

atttctga 368

<210> 300
<211> 350
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 300

cgccatcgac ggtgccgacg aggttgaccc tgaccttaac cttgtgaaag ggaggggtgg 60

tgctcttctt cgtgagaaga tggttgaggc agcatcggac aagtttattg ttattgttga 120

cgagacaaaa ctagttgatg ggttaggagg tagtggtcta gccatgccag tggaagttgt 180

gcagttctgc tggaagtaca accttgtaag attgcaggaa ctgtttaagg aggaaggagt 240

cgaggcaaag ctaaggtttg aaggcgacaa gccctatgtt actgacaact ncaactacat 300

cgtcgattta tacttcaaga cgccaatcaa ggatgcgttg gcagcaggac 350

<210> 301
<211> 264

<212> DNA
<213> Zea mays

<400> 301

ccgctctcca cgctcgacga caacccgctc atcgacctcg ccatcgacgg tgccgacgag 60

gttgaccctg acctcaacct tgtgaaaggg cggggtggtg ctcttcttcg tgagaagatg 120

gttgaggcag catcggacaa gtttattgtt attgttgacg agacaaaact agttgatggg 180

ttaggaggta gtggtctagc catgccagtg gaagttgtgc agttctgctg gaagtacaac 240

cttgtaagat tgcaggaact gttt 264

<210> 302
<211> 267
<212> DNA
<213> Zea mays

<400> 302

caaactgcgg ctgctgtaga tacgcgcgcc gtcactccaa ggtccaagcc tcccttgctc 60

ccgccaccgc ccctcaccat gggcagcgcc gccgcctctc cgcagccgtc tgggaatctg 120

acgcaggacg agctcaagcg cgtggcggcg caccgcgcgg tggagttcgt ggagcccggc 180

atgacgctgg gcctgggcac gggttccacg gccgcgcacg cgctggaccg tctgggctac 240

ctactccgcg tgggctcgct gtccggg 267

<210> 303
<211> 333
<212> DNA
<213> Zea mays

<400> 303

acgcccacgc gtccgtcccg ttcccgatcc tcatcacctc aaccccgcgc cgccccctcc 60

ccaccaccct cgccatggtc agcgccgccg cctcgccgcc gccgtccggg aagccgacgc 120

aggacgagct gaagcgcttg gcggcgcacc gcgcggtgga gctcgtggag cccggcatga 180

cgctgggcct gggcacgggc tccacggcgg cgcacgcgct ggaccgcctg ggcgacctcc 240

tccgcgcggg cgcgctgccg gggtggccg gcgtgccgac ctcgctcaag acggatgcgc 300

aagcggcgcg cgtcggcatc ccgctgctcc cgc 333

<210> 304
<211> 420
<212> DNA
<213> Zea mays

<400> 304

ggcgtgccca catccaagcg caccttcgag caggcgcagt cgctcggcat cccgctctgg 60

acgctcgacg acaacccgct catcgacctc gccatcgacg gtgccgacga ggttgaccct 120

gacctcaacc ttgtgaaagg gcggggtggt gctcttcttc gtgagaagat ggttgaggca 180

gcatcggaca agtttattgt tattgttgac gagacaaaac tagttgatgg gttaggaggt 240

agtggtctag ccatgccagt ggaagttgtg cagttctgct ggaagtacaa ccttgtaaga 300

ttgcaggaac tgtttaagga ggaaggagtc gaggcaaagc taaggtttga aggcgacaag 360

ccctatgtta ctgacaactc aaactacatc gtcgatttat acttcaagac gccaatcaag 420

<210> 305
<211> 432
<212> DNA
<213> Zea mays

<400> 305

accttgtgaa agggcggggt ggtgctcttc ttcgtgagaa gatggttgag gcagcatcgg 60

acaagtttat tgttattgtt gacgagacaa aactagttga tgggttagga ggtagtggtc 120

tagccatgcc agtggaagtt gtgcagttct gctggaagta caaccttgta agattgcagg 180

aactgtttaa ggaggaagga gtcgaggcaa agctaaggtt tgaaggcgac aagccctatg 240

ttactgacaa ctcaaactac atcgtcgatt tatacttcaa gacgccaatc aaggatgcgt 300

tggcagcagg acaggaaatt gcagctctgg aaggagttgt tgaccatggg ttgttcttga 360

acatggcgag ttcagtgatc attgctggaa cggacggtgt cagtgtcaaa acgaagtgag 420

tttttgagtt gc 432

<210> 306
<211> 461
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 306

caccaagcat gccgcnnatg gggtgntgtt nttcgtgaga agatgggtga ggcagcatng 60

gacaagttta ntgttattgt tgacgagaca aaactagttg atgggttagg aggtagtggt 120

ctagccatgc cagtggaagt tgtgcagttc tgctggaagt acaaccttgt aagattgcag 180

gaactgttta aggaggaagg agtcgaggca aagctaaggt ttgaaggcga caagccctat 240

gttactgaca actcaaacta catcgtcgat ttatacttca agacgccaat caaggatgcc 300

gttggcagca ggacaggaaa ttgcagctct ggaaggagtt gttgaccatg ggttgttctt 360

gaacatggcg agttcagtga tcattgctgg aacggacggt gtcagtgtca aaacgaaatg 420

agtttttgag ttgctttgtt ggttgngttg aaattttttt t 461

<210> 307
<211> 249
<212> DNA
<213> Glycine max

<400> 307

ctcgatctcg ccatcgacgg cgccgacgag gtcgaccccg acctcaacct cgtcaaaggc 60

cgcggcggcg ccctcctccg cgagaagatg gtcgaggccg cctccgacaa gttcgtcgtg 120

gtcgtcgacg acaccaagct cgtggacggc ctcggcggaa gcgggctggc catgccggtg 180

gaggtggtcc agttctgctg gaagtacaat ctggatcggc ttcaggagct tttcaaggaa 240

gaaggtgtg 249

<210> 308
<211> 240
<212> DNA
<213> Glycine max

<400> 308

gtcgaccccg acctcaacct cgtcaaaggc cgcggcggcg ccctcctccg cgagaagatg 60

gtcgaggccg cctccgacaa gttcgtcgtg gtcgtcgacg acaccaagct cgtggacggc 120

ctcgcggaag cgggctggcc atgccggtgg aggtggtcca gttctgctgg aagtacaatc 180

tggatcggct tcaggagctt ttcaaggaag aaggtgtgga agcaaaattg agattggagg 240

<210> 309
<211> 262
<212> DNA

<213> Glycine max

<400> 309

ggtcgacccc gacctcaacc tcgtcaaagg ccgcggcggc gccctcctcc gcgagaagat 60

ggtcgaggcc gcctccgaca agttcgtcgt ggtcgtcgac gacaccaagc tcgtggacgg 120

cctcggcgga agcgggctgg ccatgccggt ggaggtggtc cagatctgct ggaagtacaa 180

tctggatcgg cttcaggagc ttttcaagga agaaggtgtg gaagcaaaat tgagattgga 240

ggagagtggg aaccctacgt ca 262

<210> 310
<211> 263
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 310

accacacatt caattttana cctctgggcg tggctagctt caacctttaa cattaacatg 60

gccattccct acccccattt catcgccacc gagaaagccg ccatggacgc cggcctcctc 120

cacccctcct ccccctccgt catcctcacc caagacgatt tgaagaaaat cgccgcctac 180

aaggccgtcg agtacgtgga gtccggcatg atcctcggcc tcggcaccgg ctccaccgcc 240

aagcatgccg tcgaccgcat cgg 263

<210> 311
<211> 274
<212> DNA
<213> Glycine max

<400> 311

cttacattcc tttctccacc acacattcaa ttttgaacct ctgggactgg ctagcttcaa 60

cctttaacat taacatggcc attccctacc cccatttcat cgccaccgag aaagccgcca 120

tggacgccgg cctcctccac ccctcctccc cctccgtcat cctcacccaa gacgatttga 180

agaaaatcgc cgcctacaag gccgtcgagt acgtggagtc cggcatggtc ctcggcctag 240

gcaccggctc caccgccaag catgccgtcg accg 274

<210> 312
<211> 333

<212> DNA
<213> Zea mays

<400> 312

ctcacctccc ctccactccc tttctcccct gactcctgct ctataggatc ctccgcctcc 60

atcgcctctc gcgcctccaa tcgccttcgg cgcttcgtcc gtcctgctcc acctcttctt 120

acgccggttg accctgacct caaccttgtg aaagggcggg gtggtgctct tcttcgtgag 180

aagatggttg aggcagcatc ggacaagttt attgttattg ttgacgagac aaaactagtt 240

gatgggttag gaggtagtgg tctagccatg ccagtggaag ttgtgcagtt ctgctggaag 300

tacaaccttg taagattgca ggactgttaa gga 333

<210> 313
<211> 302
<212> DNA
<213> Zea mays

<400> 313

ggatggtgct cgggctcggg acgggctcca cggccgcctt cgccgtcgcc gagatcggcg 60

cgctcctggc cgcgggcaag ctcgagaaga tcgtcggcgt gcccacatcc aagcgcacct 120

tcgagcaggc gcagtcgctc ggcatcccgc tctccacgct cgacgacaac ccgctcatcg 180

acctcgccat cgacggtgcc gacgaggttg accctgacct caaccttgtg aaagggcggg 240

gtggtgctct tcttcgtgag aagatggttg aggcagcatc ggacaagttt attgttattg 300

tt 302

<210> 314
<211> 244
<212> DNA
<213> Glycine max

<400> 314

ctcaaggaca tcgtcggaat ccccacctcc acaaaaaccc acgaacaagc cctctccctc 60

gggatccccc tctccgatct cgacgcccac cccgccatcg atctcgccat cgacggcgcc 120

gacgaggtcg atcccttcct caacctcgtc aagggccgtg gcggctccct cctccgagaa 180

aaaatggtcg aaggcgcatg caagaagttc atcgtcatcg ttgatgagtc caagctcgta 240

aact 244

<210> 315
<211> 267
<212> DNA
<213> Glycine max

<400> 315

ccgccatcga tctcgccatc gacggcgccg acgaggtcga ccccttcctc aacctcgtca 60

agggccgtgg cggctccctc ctccgagaaa aaatggtcga aggcgcatgc aagaagttca 120

tcgtcatcgt tgatgagtcc aagctcgtaa actatttggg gggtagtggg ttggccatgc 180

ccgttgaggt tattaagttc tgttggaggt tcaccgcggc gaggttgcag aagcttcttg 240

aggaggctgg gtgcgttgcc aggctca 267

<210> 316
<211> 291
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 316

gatttgaaga aaatcgcngc ctacaaggcc gtcgagtacg tggagtccgg catggtcctc 60

ggcctaggca ccggctccan cgccaagcat gccgtcganc gcatcggcga gctcctccgc 120

cagggcaagc tcaaggacat cgtcggaatc cccacctcca caaaaaccca cgaacaagcc 180

ctctccctcg ggatccccct ctccgatctc gacgcccacc ccgccatcga tctcgccatc 240

gacggcgccg acgaggtcga ccccttcctc aacctcgtca agggccgtgg g 291

<210> 317
<211> 265
<212> DNA
<213> Glycine max

<400> 317

agacgacctc aagaaaatcg ccgcctacaa ggccgtcgag tacgtcgagt ccggcatggt 60

cctcggcctc ggcaccggct ccactgccaa gcacgccgtc gaccgcatcg gcgagctcct 120

ccgccaagga aaactcaaag acatcgtcgg catccccacc tccaccaaaa cccacgacca 180

ggccctctcc ctcggcatcc ccctctccga tctcgactcc caccccaccg tcgatctcgc 240

catcgacggc gccgacgagg tcgat 265

<210> 318
<211> 265
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 318

cacaccacna cgcctccacg ngccttattc nanncacccc taantngngt aaacngcgca 60

ctaccacncc actaccctcc ccgccatcng cgccatcacc ctcacccagg acgaccncaa 120

gagactcgcc gccgacaagg ccgtggagtc cgtcaagagc ggcatggtcc tcggcctagg 180

caccggctcc actgctgcct tcgtcgtcgc caagcttggc gcccttctcg cctccggcca 240

actctccgac atcgtcggtg tcccc 265

<210> 319
<211> 320
<212> DNA
<213> Zea mays

<400> 319

gagaagtcgg tcaacacgat ccggttcctg gccatcgacg ccgtcgagaa ggccaactcc 60

ggccacccgg gcctccccat gggctgcgcg cccatgggcc acgtcctcta cgacgaggtc 120

atgcgctaca accccaagaa cccctactgg ttcaaccgcg accgcttcgt cctctccgcc 180

ggccacggct gcatgctcca gtacgccctc ctccacctcg ccggttacga cagcgttaag 240

gaggaggact tgaagcagtt ctggcaatgg ggaagcagaa caccgggcca ccctgagaac 300

tttgagactc caggagttga 320

<210> 320
<211> 235
<212> DNA
<213> Zea mays

<400> 320

gtacaccatc tctgacaact ctaccggcaa caagccgggc atcattgtga tgggcaccgt 60

ctccgagctg tagatcgcgg ccaaggccgt cgacgagctg aggaaggagg ggaagacggt 120

ccgcgtcgtc tcgttcgtct cctgggaact ctttgatgag cagtcggatg agcacaagga 180

gatcgtcctc cctgccgccg tcacagcgag gatcagcatc gaagccgggt ccact 235

<210> 321
<211> 276
<212> DNA
<213> Zea mays

<400> 321

ccagattcgc ttaaggctga aaggcggatg gaagctctca tatagtcggt gaagacaaag 60

aacgttgcac aataaggtat cagaccaggg ctgtgaacag cgatgccatt cgaaatggca 120

cccatagcat gctctcgcac accgaagcga atgtttctct cttcaggagt atccctctgg 180

atttctccaa acttcttaag cagtgtcatg tttgacgttg cgagatccga actacctcca 240

agaaatccag gtattacttt ggcaagtgca ttcaag 276

<210> 322
<211> 292
<212> DNA
<213> Zea mays

<400> 322

gcaaccaggc agaaccttgg atggccctat gacacattct ttgtaccaga ggacgtcaag 60

agtcactgga gccgccacac acccgaaggt gctgcacttg aggctgattg gaacgctatg 120

tttgcagagt acgagaagaa gtatgcagat gatgcagcaa ccttgaaaag tatcatcacg 180

ggggagttac ccactggctg ggttgatgct cttcctaaat acactccaga gagcccagga 240

gatgccacca ggaacctctc ccagcagtgc ctgaacgcgc ttgctaatgt tg 292

<210> 323
<211> 295
<212> DNA
<213> Zea mays

<400> 323

tggaagtgca ctgggtgcca aagaggttga agcaaccagg cagaaccttg gatggcccta 60

cgacacattc tttgtaccag aggacgtcaa gagtcactgg agccgccaca cacccgaagg 120

tgctgcactt gaggctgatt ggaacgctaa gtttgcagag tacgagaaga agtatgcaga 180

tgatgcagca accttgaaaa gtatcatcac gggggagtta cccactggct gggttgatgc 240

tcttcctaaa tacactccag agagcccagg agatgccacc taggaactct cccag 295

<210> 324
<211> 285
<212> DNA
<213> Zea mays

<400> 324

agagtacgag aagaagtatg cagatgatgc agcaaccttg aaaagtatca tcacggggga 60

gttacccact ggctgggttg atgctcttcc taaatacact ccagagagcc caggagatgc 120

caccaggaac ctctcccagc agtgcctgaa cgcccttgct aatgttgtgc ctggtcttat 180

cggaggcagt gctgatcttg catcctccaa catgactctg ctgaagatgt ttggtgactt 240

ccagaaggat acagctgaag agcgcaatgt ccgcttcgga gtcag 285

<210> 325
<211> 296
<212> DNA
<213> Zea mays

<400> 325

ggccacagtc aaggagccgg acacaccgaa gcggagcacc tgaggccgat tggaacgcta 60

tgtttgcaga gtacgagaag aagtatgcag atgatgcagc aaccttgaaa agtatcatca 120

cgggggagtt acccactggc tgggttgatg ctcttcctaa atacactcca gagagcccag 180

gagatgccac caggaacctc tcccagcagt gcctgaacgc gcttgctaat gttgtgcctg 240

gtcttattgg aggcagtgct gatcttgcat cctccaacat gactctgctg aagatg 296

<210> 326
<211> 293
<212> DNA
<213> Zea mays

<400> 326

caggagatgc caccaggaac ctctcccagc agtgcctgaa cgcgcttgct aatgttgtgc 60

ctggtcttat tggaggcagt gctgatcttg catcctccaa catgactctg ctgaagatgt 120

ttggtgactt ccagaaggat acagctgaag agcgcaatgt ccgctttgga gtcagagagc 180

acggaatggg cgccatttgc acaggcattg ctctgcacag cccagggttt gttccgtact 240

gtgctacagt ctttgtcttc actgtttaca tgagaggtgc catgaggatc tcg 293

<210> 327
<211> 271
<212> DNA
<213> Zea mays

<400> 327

gtcaagagtc actggagccg ccacacaccc gaaggtgctg cacttgaggc tgattggaac 60

gctatgtttg cagagtacga gaagaagtat gcagatgatg cagcaacctt gaaaagtatc 120

atcacggggg agttacccac tggctgggtt gatgctcttc ctaaatacac tccagagagc 180

ccaggagatg ccaccaggaa cctctcccag cagtgcctga acgcgcttgc taatgttgtg 240

cctggtctta ttggaggcag tgctgatctt g 271

<210> 328
<211> 285
<212> DNA
<213> Zea mays

<400> 328

ccaccaggac cctctcccag cagtgcctga acgcgcttgc taatgttgtg cctggtctta 60

ttggaggcag tgctgatctt gcatcctcca acatgactct gctgaagatg tttggagact 120

tccagaagga tacagctgaa gagcgcaatg tccgctttgg agtcagagag cacggaatgg 180

gcgccatttg caacggcatt gctctgcaca gcccagggtt tgttccgtac tgtgctacat 240

tctttgtctt cactgattac atgagaggtg ccatgaggat ctcgg 285

<210> 329
<211> 274
<212> DNA
<213> Zea mays

<400> 329

ctcgagcgaa tcggctcgag atcacggggg agttacccac tgcctgggtt gatgctcacc 60

ctaaatacac tccagagagc ccaggagatg ccaccaggaa cctctcccag cagtgcctga 120

acgcccttgc taatgttgtg cctggtctta tcggaggcag tgctgatctt gcatcctcca 180

acatgactct gctgaagatg tttggtgact tccagaagga tacagctgaa gagcgcaatg 240

tccgcttcgg agtcagagag cacggaatgg gcgc 274

<210> 330
<211> 187
<212> DNA
<213> Zea mays

<400> 330

ccactggctg ggttgatgct cttcctaaat acactccaga gagcccagga gatgccacca 60

ggaacctctc ccagcagtgc ctgaacgccc ttgctaatgt tgtgcctggt cttatcggag 120

gcagtgctga tcttgcatcc tccaacatga ctctgctgaa gatgtttggt gacttccaga 180

aggatac 187

<210> 331
<211> 219
<212> DNA
<213> Zea mays

<400> 331

gaagtatgca gatgatgcag caaccttgaa aagtatcatc acgggggagt tacccactgg 60

ctgggttgat gctcttccta aatacactcc agagagccca ggagatgcca ccaggaacct 120

ctcccagcag tgcctgaacg cgcttgctaa tgttgtgcct ggtcttattg gaggcagtgc 180

tgatcttgca tcttccaaca tgactctgct gaagatgtt 219

<210> 332
<211> 177
<212> DNA
<213> Zea mays

<400> 332

tcttattgga ggcagtgctg atcttgcatc ctccaacatg actctgctga agatgtgggg 60

tgactcccag aaggatacac tgaagagcgc aatgtccgct ttggagtcag agagcacgga 120

atgggcgcca tttgcaacgg cattgctctg cacagcccag ggtttgttcc gtactgt 177

<210> 333
<211> 261
<212> DNA
<213> Zea mays

<400> 333

cgctcgagcg catcggctcg agatcacggg ggagttaccc actggctggg ttgatgctat 60

tcctaaatac actccagaga gcccaggagc tgccacagga ccctctccca gcagtgcctg 120

aacgcccttg ctaatgttgt gcctggtctt atcggaggca gtgctgatct tgcatcctcc 180

aacatgactc tgctgaagat gtttggtgac ttccagaagg atacagctga agagcgccat 240

gtccgcttcg gagtcagaga g 261

<210> 334
<211> 203
<212> DNA
<213> Zea mays

<400> 334

caggggtctt ggcaagctga tagctttcta cgatgacaac cacatttcca tcgacggaga 60

cacggagatt gcattcacag aggacgtgag cacccgcttc gaggctcttg ggtggcacac 120

gatctgggtt aagaatggga acaccggata tgatgacatc cgcgcaccat taaggaggcg 180

aaggcagtca ctgacaagcc cac 203

<210> 335
<211> 289
<212> DNA
<213> Zea mays

<400> 335

gagcgcaatg tccgcttcgg agtcagagag cacggaatgg gcgccatttg caacggcatt 60

gctctgcaca gcccagggtt tgttccgtac tgtgctacat tctttgtctt cactgattac 120

atgagaggtg ccatgaggat ctcggccctg tctgaagccg gagtcatcta tgtcatgacc 180

cacgactcta ttggtctcgg agaagatggc ccgacccatc agcccatcga gcacctggtg 240

agcttccgtg cgatgccgaa catactgatg ctccgccctg ctgatggca 289

<210> 336
<211> 305
<212> DNA
<213> Zea mays

<400> 336

gatgtttggt gacttccaga aggatacagc tgaagagcgc aatgtccgct tcggagtcag 60

agagcacgga atgggcgcca tttgcaacgg cattgctctg cacagcccag ggtttgttcc 120

gtactgtgct acattctttg tcttcactga ttacatgaga ggtgccatga ggatctcggc 180

cctgtctgaa gccggagtca tctatgtcat gacccacgac tctattggtc tcggagaaga 240

tggcccgacc catcagccca tcgagcacct ggtgagcttc cgtgcgatgc cgaacatact 300

gatgc 305

<210> 337
<211> 275
<212> DNA
<213> Zea mays

<400> 337

attacatgag aggtgccatg aggatctcgg ccctgtctga agccggagtc atctatgtca 60

tgacccacga ctctattggt ctcggagaag atggcccgac ccatcagccc atcgagcacc 120

tggtgagctt ccgtgcgatg ccgaacatac tgatgctccg ccctgctgat ggcaacgaga 180

ctgccggagc atacaaagtc gcggtcctca acaggaagag gccgtccatc ctcgctctct 240

ccaggcaaaa gctccctcac ctgcctggca cctcg 275

<210> 338
<211> 288
<212> DNA
<213> Zea mays

<400> 338

agcacctggt gagcttccgt gcgatgccga acatactgat gctccgccct gctgatggca 60

acgagactgc cggagcatac aaagtcgcgg tcctcaacag gaagaggccg tccatcctcg 120

ctctctccag gcaaaagctc cctcacctgc ctggcacctc gatcgagggc gtggagaagg 180

gcgggtacac catctctgac aactcgaccg gcaacaagcc tgacatcatt gtgatgggca 240

ccggctccga gctggagatc gcggccaagg ccgccgacga gctgagga 288

<210> 339
<211> 280
<212> DNA
<213> Zea mays

<400> 339

ctgccggagc atacaaagtc gcggtcctca acaggaagag gccgtccatc ctcgctctct 60

ccaggcaaaa gctccctcac ctgcctggca cctcgatcga gggcgtggag aagggcgggt 120

acaccatctc tgacaactcg accggcaaca agcctgacat cattgtgatg ggcaccggct 180

ccgagctgga gatcgcggcc aaggccgccg acgagctgag gaaggagggg aagacggtcc 240

gcgtcgtctc gttcgtctcc tgggaactct ttgatgagca 280

<210> 340
<211> 255
<212> DNA
<213> Zea mays

<400> 340

gtctcggaga agatggcccg acccatcagc ccatcgagca cctggtgagc ttccgtgcga 60

tgccgaacat actgatgctc cgccctgctg atggcaacga gactgccgga gcatacaaag 120

tcgcggtcct caacaggaag aggccgtcca tcctcgctct ctccaggcaa aagctccctc 180

acctgcctgg cacctcgatc gagggcgtgg agaagggcgg gtacaccatc tctgacactc 240

gaccggcaac aagcc 255

<210> 341
<211> 254
<212> DNA
<213> Zea mays

<400> 341

catctatgtc atgacccacg actctattgg tctcggagaa gatggcccga cccatcagcc 60

catcgagcac ctggtgagct tccgtgcgat gccgaacata ctgatgctcc gccctgctga 120

tggcaacgag actgccggag catacaaagt cgcggtcctc aacaggaaga ggccgtccat 180

cctcgctctc tccaggcaaa agctccctca cctgcctggc acctcgatcg agggcgtgga 240

gaagggcggg taca 254

<210> 342
<211> 273
<212> DNA
<213> Zea mays

<400> 342

ggagatcgcg gccaaggccg ccgacgagct gaggaaggag gggaagacgg tccgcgtcgt 60

ctcgttcgtc tcctgggaac tctttgatga gcagtcggat gagtacaagg agagcgtcct 120

ccctgccgcc gtcacagcga ggatcagcat cgaggccggg tccactctcg gctggcagaa 180

gtacgtcgga gcccagggca aggccattgg catcgacaag ttcggcgcga gtgctcctgc 240

cgggacgatc tacaaggagt acggcatcac cgt 273

<210> 343
<211> 301
<212> DNA
<213> Zea mays

<400> 343

ctatgtcatg acccacgact ctattggtct cggagaggat ggcccgaccc atcagcccat 60

cgagcacctg gtgagcttcc gtgcgatgcc gaacatactg atgctccgcc ctgctgatgg 120

caacgagact gccggagcat acaaagtcgc ggtcctcaac aggaagaggc cgtccatcct 180

cgctctctcc aggcaaaagc tccctcacct gcctggcacc tcgatcgacg gcgtggagaa 240

tggcgggtac accatctctg acaactcgac cggcaacaag cctgacctca ttgtgatggg 300

c 301

<210> 344
<211> 276
<212> DNA
<213> Zea mays

<400> 344

gcctgacatc attgtgatgg gcaccggctc cgagctggag atcgcggcca aggccgccga 60

cgagctgagg tcatgagggg aagacggtcc gcgtcgtctc gttcgtctcc tgggaactct 120

ttgatgagca gtcggatgag tacaaggaga gcgtcctccc tgccgccgtc acagcgagga 180

tcagcatcga ggccgggtcc actctcggct ggcagaagta cgtcggagcc cagggcaagg 240

ccattggcat cgacaagttc ggcgcgagtg ctcctg 276

<210> 345
<211> 300

<212> DNA
<213> Zea mays

<400> 345

cgacgagctg aggaaggagg ggaagacggt ccgcgtcgtc tcgttcgtct cctgggaact 60

ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgccgccg tcacagcgag 120

gatcagcatc gaggccgggt ccactctcgg ctggcagaag tacgtcggag cccagggcaa 180

ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct acaaggagta 240

cggcatcacc gtggagagca tcattgcagc tgccaagagc ttttaagagc taacaacggt 300

<210> 346
<211> 316
<212> DNA
<213> Zea mays

<400> 346

ggtgccatga ggatctcggc cctgtctgaa gccggagtca tctatgtcat gacccacgac 60

tctattggtc tcggagagga tggcccgacc catcagccca tcgagcacct ggtgagcttc 120

cgtgcgatgc cgaacatact gatgctccgc cctgctgatg gcaacgagac tgccggagca 180

tacatcgccg cggtcctcaa caggaagagg ccgtccatcc tcgctctctc caggcaaaag 240

ctccctcacc tgcctggcac ctcgatcgag ggcgtggaga agggcgggta caccatctct 300

gacaactcga ccggca 316

<210> 347
<211> 299
<212> DNA
<213> Zea mays

<400> 347

ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgctgccg tcacagcgag 60

gatcagcatc gaggccgggt ccactcttgg ctggcagaag tacgtcggag cccagggcaa 120

ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct acaaggagta 180

cggcatcacc gtggagagca tcattgcagc tgccaagagc ttttaagagc taacaacggt 240

ctggagtttt ttttattgtc gtcgttgatg ccaaaggaac actgtacctt gaggacagt 299

<210> 348
<211> 242
<212> DNA
<213> Zea mays

<400> 348

caggcgtcct ccctgctgcc gtcacagcga ggatcagcat cgaggccggg tccactcttg 60

gctggcagaa gtacgtcgga gcccagggca aggccattgg catcgacaag ttcggcgcga 120

gtgctcctgc cgggacgatc tacaaggagt acggcatcac cgtggagagc atcattgcag 180

ctgccaagag cttttaagag ctaacaacgg tctggagttt tttttattgt cgtcgttgat 240

gc 242

<210> 349
<211> 287
<212> DNA
<213> Zea mays

<400> 349

tctcgagccg gtcctcaaca ggaagaggcc gtccatcctc gctctctcca ggcaaaagct 60

ccctcacctg cctggcacct cgatcgaggg cgtggagaag ggcgggtaca ccatctctga 120

caactcgacc ggcaacaagc ctgacatcat tgtgatgggc accggctccg agctggagat 180

cgcggccaag gccgccgacg agctgaggaa ggaggggaag acggtccgcg tcgtctcgtt 240

cgtctcctgg gaactctttg atgagcagtc ggatgagtac aaggaga 287

<210> 350
<211> 265
<212> DNA
<213> Zea mays

<400> 350

gtccactctc ggctggcaga agtacgtcgg agcccagggc aaggccattg gcatcgacaa 60

gttcggcgcg agtgctcctg ccgggacgat ctacaaggag tacggcatca ccgtggagag 120

catcattgca gctgccaaga gcctttaaga gctaacaacg gtctggagtt tttcttattg 180

tcgtcgttga tgccaaagga acactgtacc tagaggacat cctatgcctc ggagcttgga 240

ataatgatga tggagggagc ggaag 265

<210> 351
<211> 336
<212> DNA
<213> Zea mays

<400> 351

cttcgaggct cttgggtggc acacgatctg ggttaagaat gggaacaccg gatatgatga 60

catccgcgca ccattaagga ggcgaaggca gttactgaca agcccacctt gatcaaggtg 120

actaccacga tcggttttgg atctcccaac aaggccaact catacagtgt tcatggaagt 180

gcactgggtg ccaaataggt tgaagcaacc aggcagaacc ttggatggcc ctatgacaca 240

ttctttgtac cagaggacgt caagagtcac tggagccgcc acacacccga aggtgctgca 300

cttgaggctg attggaacgc taagtttgca gagtac 336

<210> 352
<211> 275
<212> DNA
<213> Zea mays

<400> 352

tgatcacccg cttcgaggct cttgggtggc acactatctg ggttaagaat gggaacaccg 60

gatatgatga catccgcaca ccattaagga ggcgaaggca gttactgaca agcccacctt 120

gatcaaggtg actaccacat cggttttgga tctcccaaca aggccaactc atacagtgtt 180

tatggaagtg cactgggtgc caaagaggtt gaagcaacca ggcagaacct tggatggccc 240

tatgacacat tctctgtacc agaggacgtc aagag 275

<210> 353
<211> 286
<212> DNA
<213> Zea mays

<400> 353

ccggatatga tgacatccgc gcaccattaa ggaggcgaag gcagttactg acaagcccac 60

cttgatcaag gtgactacca cgatcggttt tggatctccc aacaaggcca actcatacag 120

tgttcatgga agtgcactgg gtgccaaaga ggttgaagca accaggcaga accttggatg 180

gccctatgac acattctttg taccagagga cgtcaagagt cactggagcc gccacacacc 240

cgaacgtgct gcacttgagg ctgattggaa cgctaagttt gcagag 286

<210> 354
<211> 249
<212> DNA
<213> Zea mays

<400> 354

cttgggtggc acacgatctg ggttaagaat gggaacaccg gatatgatga catccgcgca 60

ccattaagga ggcgaaggca gttactgaca agcccacctt gatcaaggtg actaccacga 120

tcggttttgg atctcccaac aaggccaact catacagtgt tcatggaagt gcactgggtg 180

ccaaagaggt tgaagcaacc aggcagaacc ttggatggcc ctatgacaca ttctttgtac 240

cagaggacg 249

<210> 355
<211> 423
<212> DNA
<213> Zea mays

<400> 355

agctccctca cctgcctggc acctcgatcg agggcgtgga gaagggcggg tacaccatgt 60

ctgacaactc gaccggcaac aagcctgacc tcattgtgat gggcaccggc tccgagctgg 120

agatcgcggc caaggccgcc gacgagctga ggaaggaggg caagacggtc cgcgtcgtct 180

cgttcgtctc ctgggaactc tttgatgagc agtcggatga gtacaaggag agcgtcctcc 240

ctgctgccgt cacagcgagg atcagcatcg aggccgggtc cactcttggc tggcagaagt 300

acgtcggagc ccagggcaag gccattggca tcgacaagtt cggcgcgagt gctcctgccg 360

ggacgatcta caaggagtac ggcatcaccg tggagagcat cattgcagct gccaagaagc 420

ttt 423

<210> 356
<211> 385
<212> DNA
<213> Zea mays

<400> 356

caaccggcac caagcctgac atcattgggt tgggcaccgg ctccgagctg gagatcgcgg 60

gcaatgcggc cgacgagctg aggaaggagg ggaagacggt ccgcgtcgtc tcgttcgtct 120

cctgggaact ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgccgacg 180

tcacagcgag gatcagcatc gaggccgggt ccactctcgg ctggcagaag tacgtcggag 240

cccaaggcaa ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct 300

acaaggagta cggcatcacc gtggagagca tcattgcaac tgccaagagc ttttaagagc 360

taacaacggt ctgggagttt ttttt 385

<210> 357
<211> 279
<212> DNA
<213> Glycine max

<400> 357

atgctaagtt tgctgagtat gaaaagaaat acaaggagga agctgcagaa ttgaaatcta 60

ttatcaatgg tgaattccct gctggttggg agaaagcact tccgacatac actccagaga 120

gcccagcgga tgccaccaga aacctgtctc aaacaaacct taatgccctt gcaaaggttc 180

ttcccggtct gcttggtggc agtgcagatc ttgcttcttc caacatgacc ttgctcaaaa 240

tgttcgggga cttccagaag gatactccag cagagcgta 279

<210> 358
<211> 246
<212> DNA
<213> Glycine max

<400> 358

ccttgctcaa aatgttcggg gacttccaaa aggatactcc agcagagcgt aatgttagat 60

tcggtgttag agaacacgga atgggagcta tctgcaacgg cattgctctt cacagccctg 120

gactgattcc atattgtgca accttctttg tattcactga ctacatgaga ggtgccataa 180

ggctttctgc gctgtctgag gctggggtta tttatgtcat gacccatgat tcaataggac 240

ttggag 246

<210> 359
<211> 220
<212> DNA
<213> Glycine max

<400> 359

caataaccag tgagagtcac aatcaaatag tagggaatgg gttaatcctt ggaacagggc 60

tgattccata ttgtgcaacc ttctttgtat tcactgacta catgagaggt gccataaggc 120

tttctgcgct gtctgaggct ggggttattt atgtcatgac ccatgattca ataggacttg 180

gagaagatgg gccaacccac cagcctattg agcacctagc 220

<210> 360
<211> 263
<212> DNA
<213> Glycine max

<400> 360

cagaaacctg tctcaaacaa accttaatgc ccttgcaaag gttcttcccg gtctgcttgg 60

tggcagtgca gatcttgctt cttccaacat gaccttgctc aaaatgttcg gggacttcca 120

aaaggatact ccagcagagc gtaatgttag attcggtgtt agagaacacg gaatgggagc 180

tatctgcaat ggcattgctc ttcacagccc tggactgatt ccatattgtg caaccttctt 240

tgtattcact gactacatga gag 263

<210> 361
<211> 308
<212> DNA
<213> Glycine max

<400> 361

tccttcccat cattctctgg cctcaagtca cattctacat gcaaagcagc agcagccacg 60

tcctcgcgta gaaggggtgc ttgtccatcc accaacgttg ttcgagccgc tgcggttgag 120

acactcgacc aaaccaccga ggtttctctg gtggagaaat ccgtcaacac cattcggttt 180

ttggccattg atgcagttga gaaggccaac tctggtcacc ctggtctccc catggggtgt 240

gctccaatgg gtcacattct ctacgatgag ataatgaggt acaatcctaa gaaccccgtt 300

ggttcaac 308

<210> 362
<211> 263
<212> DNA
<213> Glycine max

<400> 362

tgctgtttca gccagagtta gcattgaggc aggatcaaca tttgggtggg agaaaattgt 60

tggagcaaaa gggaaaagca ataggcattg atcgttttgg agctagtgct ccagctggaa 120

gaatatacaa agaatttggt atcactaagg aagctgttgt tgctgcagct aaagagctta 180

tctagaactt ttgatttttt ttgccttctg gttttggttg agagcattcc atgtcatgaa 240

taagaaaaag gttaaatatc ctt 263

<210> 363
<211> 332
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 363

aaccattggt tatggttctc ctaacaaggc taactcctac agtgtgcatg gaagtgcact 60

gggtgccaaa gaagttgang ccacaaggca gaaccttgga tggtcacatg agccattcca 120

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga 180

agctgaatgg aatgctaagt ttgctgagta tgaaaagaat acaaggagga agctgcagaa 240

ttgaaatcta ttatcaatgg tgaattccct gctggttggg agaaagcact tccgacatac 300

actccagaga gcccacgggt gccaccagaa ac 332

<210> 364
<211> 247
<212> DNA
<213> Glycine max

<400> 364

aaccattggt tatggttctc ctaacaaggc taactcctac agtgtgcatg gaagtgcact 60

gggtgccaaa gaagttgatg ccacaaggca gaaccttgga tggtcacatg agccattcca 120

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga 180

agctgaatgg aatgctaagt ttgctgagta tgaaaagaaa tacaaggagg aagctgcaga 240

attgaaa 247

<210> 365
<211> 238
<212> DNA

<213> Glycine max

<400> 365

caaggctaac tcctacagtg tgcatggaag tgcactgggt gccaaagaag ttgatgccac 60

aaggcagaac cttggatggt cacatgagcc attccacgtg cctgaggatg tcaaaaagca 120

ttggagtcgc cacacccctg agggtgctgc acttgaagct gaatggaatg ctaagtttgc 180

tgagtatgaa aagaaataca aggaggaagc tgcagaattg aaatctatta tcaatggt 238

<210> 366
<211> 253
<212> DNA
<213> Glycine max

<400> 366

gggtgccaaa gaagttgatg ccacaaggca gaaccttgga tggtcacatg agccattcca 60

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga 120

agctgagtgg aatgctaagt ttgctgagta tgaaaagaaa tacaaggagg aagctgcaga 180

attgaaatct attatcaatg gtgaattccc tgctggttgg gagaaagcac ttccgacata 240

cactccagag agc 253

<210> 367
<211> 171
<212> DNA
<213> Glycine max

<400> 367

gttctcctaa caaggctaac tcctacagtg tgcatggaag tgcactgggt gccaaagaag 60

ttgatgccac aaggcagaac cttggatggt cacatgagcc attccacgtg cctgaggatg 120

tcaaaaagca ttggagtcgc cacacccctg agggtgctgc acttgaagct g 171

<210> 368
<211> 277
<212> DNA
<213> Glycine max

<400> 368

atacgagcct ttccatgtgc cagaagatgt taaaaagcat tggagtcgcc atacccctga 60

gggtgctaaa cttgaagctg agtggaatgc caagtttgca gaatatgaga agaaatacag 120

tgaggaagct gcagagctga aggctattat tactgtgaat taccagctgg ttgggagaaa 180

gcacttccga catacactcc agaaagccct gctgatgcta caagaaatct gtctcagcaa 240

aatctaaatg cccttgttaa ggttcttcct ggtctac 277

<210> 369
<211> 268
<212> DNA
<213> Glycine max

<400> 369

gctacaagga agaatcttgg atggccatac gagcctttcc atgtgccaga agatgtcaag 60

aagcattgga gtcgccatac acctgagggt gctaaacttg aagctgagtg gaatgccaag 120

tttgtggaat atgagaagca atacagtgag gaagctgcag agctgaaggc tattattact 180

ggcgaattac cagcaagttg ggagaaagca cttccgacat acacaccaga aagccctgct 240

gatgctacaa gaaatctgtc tcagcaaa 268

<210> 370
<211> 258
<212> DNA
<213> Glycine max

<400> 370

taaagaagca aaggctgtca aagacaaacc cactttgatc aaggtaacca ctaccattgg 60

atttggttct ccaaacaagg ctaattccta cagtgttcat gggagtgcat taggtgctaa 120

agaagtggat gctacaagga agaatcttgg atggccatac gagcctttcc atgtgccaga 180

agatgtcaag aagcattgga gtcgccatac acctgagggt gctaaacttg aagctgagtg 240

gaatgccaag tttgtgga 258

<210> 371
<211> 247
<212> DNA
<213> Glycine max

<400> 371

gccatacccc tgagggtgct aaacttgaag ctgagtggaa tgccaagttt gcagaatatg 60

agaagaaata cagtgaggaa gctgcagagc tgaaggctat tattactggt gaattaccag 120

ctggttggga gaaagcactt ccgacataca ctccagaaag ccctgctgat gctacaagaa 180

atctgtctca gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtggca 240

gtgcaga 247

<210> 372
<211> 264
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 372

ggagtcgcca tacacctgag ggtgctaaac ttgaagctga gtggtntgcc aagtttgtgg 60

aatatgagaa gcaatacagt gaggaagctg cagagctgaa ggctattatt actggcgaat 120

taccagctgg ttgggagaaa cacttccgac atacacacca gaaagccctg ctgatgctac 180

aagaaatctg tctcagcaaa atctaaatgc ccttgttaag gttcttcctg gtctacttgg 240

tggtagtgca gatcttgcct cttc 264

<210> 373
<211> 245
<212> DNA
<213> Glycine max

<400> 373

gtggaatgcg aagtttgcag aatatgagaa gacatacagt gaggaagctg cagagctgaa 60

ggctattatt actggtgaat taccagctgg ttgggagaaa gcacttccga catacactcc 120

agaaagccct gctgatgcta caagaaatct gtctcagcaa aatctaaatg cccttgttaa 180

ggttcttcct ggtctacttg gtggcagtgc agatcttgcc tcttccaaca tgaccttgtt 240

gaaat 245

<210> 374
<211> 242
<212> DNA
<213> Glycine max

<400> 374

tggaatgcca agtttgcaga atatgagaag aaatacagtg aggaagctgc agagctgaag 60

gctattatta ctggtgaatt accagctggt tgggagaaag cacttccgac atacactcca 120

gaaagccctg ctgatgctac aagaaatctg tctcagcaaa atctaaatgc ccttgttaag 180

gttcttcctg gtctacttgg tggcagtgca gatcttgcct cttccaacat gaccttgttg 240

aa 242

<210> 375
<211> 246
<212> DNA
<213> Glycine max

<400> 375

gcagaatatg agaagaaata cagtgaggaa gctgcagagc tgaaggctat tattactggt 60

gaattaccag ctggttggga gaaagcactt ccgacataca ctccagaaag ccctgctgat 120

gctacaagaa atctgtctca gcaaaatcta aatgcccttg ttaaggttct tcctggtcta 180

cttggtggca gtgcagatct tgcctcttcc aacatgacct tgttgaaatc atacggagat 240

ttccaa 246

<210> 376
<211> 236
<212> DNA
<213> Glycine max

<400> 376

ggatgctaca aggaagaatc ttggatggcc atacgagcct ttccatgtgc cagaagatgt 60

caagaagcat tggagtcgcc atacacctga gggtgctaaa cttgaagctg agtggaatgc 120

caagtttgtg gaatatgaga agcaatacag tgaggaagct gcagagctga aggctattat 180

tactggcgaa ttaccagctg gttgggagaa agcacttccg acatacacac cagaaa 236

<210> 377
<211> 253
<212> DNA
<213> Glycine max

<400> 377

attggagtcg ccatacccct gagggtgcta aacttgaagc tgagtggaat gccaagtttg 60

cagaatatga gaagaaatac agtgaggaag ctgcagagct gaaggctatt attactggtg 120

aattaccagc tggttgggag aaagcacttc cgacatacac tccagaaagc cctgctgatg 180

ctacaagaaa tctgtctcag caaaatctaa atgccctttt aaggttcttc ctggtctact 240

tggtggcagt gca 253

<210> 378
<211> 250
<212> DNA
<213> Glycine max

<400> 378

acagtgttca tgggagtgcg ttaggtgcta aagaagtgga tgctacaagg tagaatctgg 60

gatggccata cgagcctttc catgtgccag aacgtgtcaa gaagcattgg agtcgccata 120

cacctgaggg tgctaaactt gaagctgagt ggaatgccaa gtttgtggaa tatgagaagc 180

aatacagtga ggaagctgca gagctgaagg ctattattac tggcgaatta ccagctggtt 240

gggagaaagc 250

<210> 379
<211> 268
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 379

aaacaaggct aattcctaca gtgttcatng gagtncatta ggtgctaaag aagncgatgc 60

tacaaggnag aatcttggat ggccatacga gcctttccat gtgccagang atgtcaagaa 120

gcattggagt cgccatacac ctgagggtgc taaacttgaa gctgagtgga atgccaagtt 180

tgtggaatat gagaagcaat acagtgaggn agctgcagag tgaaggctat tattactggc 240

gaattaccag ctggttggna nanancct 268

<210> 380
<211> 248
<212> DNA
<213> Glycine max

<400> 380

tgctaaagaa gtggatgcta caaggaagaa tcttggatgg ccatacgagc ctttccatgt 60

gccaacagat gtcaagaagc attggagtcg ccatacacct gagggtgcta aacttgaagc 120

tgagtggaat gccaagtttg tggaatatga gaagcaatac agtgaggaag ctgcagagct 180

gaaggctatt attactggcg aattaccagc tggttgggag aacgcacttc cgacatacac 240

accagaaa 248

<210> 381
<211> 167
<212> DNA
<213> Glycine max

<400> 381

tgcacttccg atctacacac cagatagccc tgctgatgct acaagaaatc tgtctcagca 60

aaatctaaat gcccttgtta aggttcttcc tggtctactt ggtggtagtg cagatcttgc 120

ctcttccaac atgaccttat tggaatcgta tggggatttc caaaaga 167

<210> 382
<211> 173
<212> DNA
<213> Glycine max

<400> 382

atgggagtgc attaggtgct aaagaagtgg atgctacaag gaagaatctt ggatggccat 60

acgagccttt ccatgtgcca gaagatgtac aagagcattg gagtcgccat acacctgagg 120

gtgctaaact tgaagctagt ggaatgccaa gtttgtggaa tatgagaagc aat 173

<210> 383
<211> 298
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 383

ttggatttgg ttctccaaac aagggctaat tcctacagtg ttcatgggag tgcattaggt 60

gctaaaagaa gtngatgcta caaggaagaa tcttggatgg ccatacgagc ctttccatgt 120

gccagaagat gtcaagaagc attggagtcg ccatacactg agggtgctaa acttgaagct 180

gagtggaatg ccaagtttgt ggaatatgag aagcaataca gtgaggaagc tgcagagctg 240

aaggctatta tactggcgat taccagctgg ttgggagaaa gcattccgac atacacac 298

<210> 384
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 384

gttagatttg gtgttagtga acatggaatg ggagcaatct gtaatggtat tgctcttcat 60

agccccggat tcattccata ctgtgcaact ttctttgtct tcactgacta catgagagct 120

gccataagga tttctgcact gtgtgaagct ggagttatnc nagtgatgac tcatgattcg 180

attggacttg gagaggatgg accaactcat cagccaatag agcacttggc aagcttcagg 240

gcaatgccaa acatttgatg cttcgtccag ctg 273

<210> 385
<211> 295
<212> DNA
<213> Glycine max

<400> 385

gttaggtttg gtgttagaga acatggattg ggagcaatct gtaacggtat tgctcttcat 60

agttccggat tcattccata ctgtgcaact ttctttgtct tcactgacta tatgagagct 120

gccataagga tttctgcact gtgtcgggct ggagttattt atgtgatgac tcatcattcg 180

attggacttg gagaggatgg accaactcat cagccaatag agtatttggc aagcttcagg 240

gcaatgcctc acactttgat gcttcgtcca gctgatgtat atgaactgct ggatc 295

<210> 386
<211> 260
<212> DNA
<213> Glycine max

<400> 386

gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtggta gtgcagatct 60

tgcctcttcc aacatgacct tattgaaatc gtatggggat ttccaaaaga atactcccga 120

agagcgcaat gttaggtttg gtgttagaga acatggaatg ggagcaatct gtaacggtat 180

tgctcttcat agccccggat tcattccata ctgtgcaact ttctttgtct tcactgacta 240

tatgagagct tccataagga 260

<210> 387
<211> 249
<212> DNA
<213> Glycine max

<400> 387

gcctcttcca acatgacctt gttgaaatca tacggagatt tccaaaagaa tactcccgaa 60

gagcgcaatg ttagatttgg tgttagagaa catggaatgg gagcaatctg taatggtatt 120

gctcttcata gccccggatt cattccatac tgtgcaactt tctttgtctt cactgactac 180

atgagagctg ccataaggat ttctgcactg tgtgaagctg gagttattta tgtgatgact 240

catgattcg 249

<210> 388
<211> 252
<212> DNA
<213> Glycine max

<400> 388

gggatttcca aaagaatact cccgaagagc gcaatgttag gtttggtgtt agagaacatg 60

gaatgggagc aatctgtaac ggtattgctc ttcatagccc cggattcatt ccatactgtg 120

caactttctt tgtcttcact gactatatga gagctgccat aaggatttct gcactgtgtg 180

aagctggagt tatttatgtg atgactcatg attcgattgg acttggagag gatggaccaa 240

ctcatcagcc aa 252

<210> 389
<211> 255
<212> DNA
<213> Glycine max

<400> 389

agcagatctt gcctcttcca acatgacctt attgaaatcg tatggggatt tccaaaagaa 60

tactcccgaa gagcgcaatg ttaggtttgg tgttagagaa catggaatgg gagcaatctg 120

taacggtatt gctcttcata gccccggatt cattccatac tgtgcaactt tctttgtctt 180

cactgactat atgagagctg ccataaggat ttctgcactg tgtgaagctg gagttattta 240

tgtgatgact catga 255

<210> 390
<211> 260
<212> DNA
<213> Glycine max

<400> 390

gggagcaatc tgtaatggta ttgctcttca tagccccgga ttcattccat actgtgcaac 60

ttttttgtc ttcactgact acatgagagc tgccataagg atttctgcac tgtgtgaagc 120

tggagttatt tatgtgatga ctcatgattc gattggactt ggagaggatg gaccaactca 180

tcagccaata gagcacttgg caagcttcag ggcaatgcca aacactttga tgcttcgtcc 240

agctgatggt aatgaaactg 260

<210> 391
<211> 238
<212> DNA
<213> Glycine max

<400> 391

ccggattcat tccatactgt gcaactttct ttgtcttcac tgactatatg agagctgcca 60

taaggatttc tgcactgtgt gaagctggag ttatttatgt gatgactcat gattcgattg 120

gacttggaga ggatggacca actcatcagc caatagagca tttggcaagc ttcagggcaa 180

tgccaaacac tttgatgctt cgtccagctg atggtaatga aactgctgga tcatacaa 238

<210> 392
<211> 248
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 392

gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtgnnc gtgcagatct 60

tgcctcttcc aacanngacc ttgttgaaat catacggaga tttccaaaag aatactcccg 120

aagagcgcaa tgttagattt ggtgttagag aacatggaat gggagcaatc tgtaatggta 180

ttgcncttca tagccccgga ttcatccata ctgtgcaact tttnttgtct tcatggacta 240

catgagag 248

<210> 393
<211> 167
<212> DNA
<213> Glycine max

<400> 393

catgacctta ttgaaatcgt attgggattt ccaaaagact actcccgaag agcgcaatgt 60

taggtttggt gttagagaac atggaatggg agcaatctgt aacggtattg ctcttcatag 120

acccggattc attccatact gtgcaacttt ctttgtcttc actgact 167

<210> 394
<211> 91
<212> DNA
<213> Glycine max

<400> 394

gactacatga gagctgccat aaggatttct gcactgtgtg aaagctggag ttatttatgt 60

gatgactcat ggattcgatt ggacttggag a 91

<210> 395
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 395

tgaattccga caatggggga gcaggactcc tggacatcct gagaactttg agacagttgg 60

aattgaagtg actacaggtc ctcttggtca gggcattgcc aatgctgttg ggttagcact 120

agctgagaaa cacttggctg cacgatttaa caagcctgac aatgagattg ttgaccatta 180

cacatatgtt atattgggtg atggttgtca aatggaggga atttcaaatg aagcatgctc 240

acttgccggt cactggggtc tagggaagct tatngcttta atgatgac 288

<210> 396
<211> 262
<212> DNA
<213> Glycine max

<400> 396

caagacctta aggaattccg acaatgggga agcagaactc ctggacatcc tgagaacttt 60

gagacccttg gagttgaagt gaccacaggt cctcttggtc agggcattgc caatgctgtt 120

ggattagcac tagctgagaa gcacttggct gcacgattta acaagcctga caatgagatt 180

gttgaccatt acacatatgt tatattgggt gatggttgtc aaatggaggg aatttcaaat 240

gaagcatgct cacttgccgg tc 262

<210> 397
<211> 279
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 397

cgcttggntc aaccntgacc gtttcgttct ctctgctgga tctggctgca tgctccaata 60

tgctctcctt cancttgctg gctatnacac tgttcaggaa caagacctta aggaattccg 120

acaatgggga agcagaactc ctggacatcc tgagaacttt gagacccttg gagttgaagt 180

gaccacaggt cctcttggtc agggcattgc caatgctgtt ggattagcat agctgagaag 240

cacttggctg cacgattaac aagcctgaca atgagatgt 279

<210> 398
<211> 254
<212> DNA
<213> Glycine max

<400> 398

tgacactgtt caggaacaag accttaagga attccgacaa tggggaagca gaactcctgg 60

acatcctgag aactttgaga cccttggagt tgaagtgacc acaggtcctc ttggtcaggg 120

cattgccaat gctgttggat tagcactagc tgagaagcac ttggctgcac gatttaacaa 180

gcctgacaat gagattgttg accattacac atatgttaat tgggtgatgg ttgtcaaatg 240

gagggaattt caaa 254

<210> 399
<211> 264
<212> DNA
<213> Glycine max

<400> 399

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt 60

ttgatcggaa ctggttcgga attggaaatc gctgccaaag ctgctgatga cctaaggaag 120

gaagggaagg ctgttagagt tgtttccctt gtttcttggg aactttttga tgagcaatca 180

gaagcctaca aggagagtgt tttccctgct gctgtttcag ccagagttag cattgaggca 240

ggatcaacat ttgggtggga gaaa 264

<210> 400
<211> 258
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 400

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt 60

ttgatcggaa ctggttcgga attggaaatc gctgccaaag ctgctgatga cctaaggaag 120

gaagggaagg ctgttagagt tgtttccctt gtttcttggg aactttttga tgagcaatca 180

gnagcctaca aggagagtgt tttccctgct gctgtttcag ccagagttag cattgaggca 240

ggatcaacat ttgggtgg 258

<210> 401
<211> 249
<212> DNA
<213> Glycine max

<400> 401

gagttgaaaa gggtggttac accatttcgg acaactccac tggcaacaag cctgatgtca 60

ttttgatcgg aactggttcg gaattggaaa tcgctgccaa agctgctgat gacctaagga 120

aggaagggaa ggctgttaga gttgtttccc ttgtttcttg ggaacttttt gatgagcaat 180

cagaagccta caaggagagt gttttccctg ctgctgtttc agccagagtt agcattgagg 240

caggatcaa 249

<210> 402
<211> 273
<212> DNA
<213> Glycine max

<400> 402

gagttgaaaa gggtggttac accatttcgg acaactccac tggcaacaag cctgatgtca 60

ttttgatcgg aactggttcg gaattggaaa tcgctgccaa agctgctgat gacctaagga 120

aggaagggaa ggctgttaga gttgtttccc ttgtttcttg ggaacttttt gatgagcaat 180

cagaagccta caaggagagt gttttccctg ctgctgtttc agccagagtt agcattgagg 240

caggatcaac atttgggtgg gagaaaattg ttg 273

<210> 403
<211> 256
<212> DNA
<213> Glycine max

<400> 403

cactcttctt cttcttcttc ttcttcactc tacaaccact aaactaagtg gttggttttg 60

gtttagtttc atttttttga agctcttaaa cttaaggctt aagccatggc atcctcatcc 120

tctctgcatc tatctcaggc ccttctggca cgtgctgtgt accttcatgg ctcttcttct 180

tctgaccgtg tctcactctc cttcccatca ttctctggcc tcaagtcaca ttctgcatgc 240

tccaatatgc tctcct 256

<210> 404
<211> 233
<212> DNA
<213> Glycine max

<400> 404

ctaaactaag tggttggttt tggtttagtt tcattttttt gaagcgctta aacttaaggc 60

ttaagccatg gcatcctcat cctctctgca tctatctcag gcccttctgg cacgtgctgt 120

gtaccttcat ggctcttctt cttctgaccg tgtctcactc tccttcccat cattctctgg 180

cctcaagtca cattctacat gcaaagcagc agtagccacg tcctcgcgta gaa 233

<210> 405
<211> 247
<212> DNA
<213> Glycine max

<400> 405

aactaagtgg ttggttttgg tttagtttca ttttttgaa gctcttaaac ttaaggctta 60

agccatggca tcctcatcct ctctgcatct atctcaggcc cttctggcac gtgctgtgta 120

ccttcatggc tcttcttctt ctgaccgtgt ctcactctcc ttcccatcat tctctggcct 180

caagtcacat tctacatgca aagcagcagc agccacgtcc tcgcgtagaa ggggtgcttg 240

tccatcc 247

<210> 406
<211> 243
<212> DNA
<213> Glycine max

<400> 406

aaacactctt cttcttcttc ttcttcttca ctctacaacc actaaactaa gtggttggtt 60

ttggtttagt ttcatttttt tgaagctctt aaacttaagg cttaagccat ggcatcctca 120

tcctctctgc atctatctca ggcccttctg gcacgtgctg tgtaccttca tggctcttct 180

tcttctgacc gtgtctcact ctccttccca tcattctctg gcctcaagtc acattctaca 240

tgc 243

<210> 407
<211> 215
<212> DNA
<213> Glycine max

<400> 407

ttttggttta gtttcattgt tctgaagctc ttaaacttaa ggcttaagcc atggcatcct 60

catcctctct gcatctatct caggcccttc tggcacgtgc tgtgtacctt catggctctt 120

cttctctgac cgtgtctcac tctccttccc atcattctct ggcctcaagt cacattctac 180

atgcaaagca gcagcagcca cgtcctcgcg tagaa 215

<210> 408
<211> 276
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 408

tcttcttctt cactctacaa ccactannct aagtggttgg ttttggttta gtttcatttt 60

tttgaagctc ttaaacttaa ggcttaagcc atggcatcct catcctctct gcatctatct 120

caggcccttc tggcacgtgc tgtgtacctt catggctctt cttcttctga ccgngtctca 180

ctctccttcc catcattctc tggcctcaag tcacattcta catgcaaagc agcancagcc 240

acgtcctcgc gtagaagggg tgcttgtcca tccacc 276

<210> 409
<211> 289
<212> DNA
<213> Glycine max

<400> 409

tcttcttctt cttcttcttc actctacaac cactaaacta agtggttggt tttggtttag 60

tttcattttt ttgaagctct taaacttaag gcttaagcca tggcatcctc atcctctctg 120

catctatctc aggcccttct ggcacgtgct gtgtaccttc atggctcttc ttcttctgac 180

cgtgtctcac tctccttccc atcattctct ggcctcaagt cacattctac atgcaaagca 240

gcagcagcca cgtcctcgcg tagaaggggt gcttgtccat ccaccaacg 289

<210> 410
<211> 221
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 410

tcttcttctt cactctacaa ccactaaact aagtggttgg ntttggttta gtttcatttt 60

tttgaagctc ttaaacttaa ggcttaagcc atggcatcct catcctctct gcatctatct 120

caggcccttc tggcacgtgc tgtgtacctt catggctctt cttcttctga ccgngtctca 180

ctctccttcc catcattctc tggcctcaag tcacattcta t 221

<210> 411
<211> 255
<212> DNA
<213> Glycine max

<400> 411

cttcttcttc ttcttcttct tcactctaca accactaaac taagtggttg gttttggttt 60

agtttcattt ttttgaagct cttaaactta aggcttaagc catggcatcc tcatcctctc 120

tgcatctatc tcaggcccctt ctggcacgtg ctgtgtacct tcatggctct tcttcttctg 180

accgtgtctc actctccttc ccatcattct ctggcctcaa gtcacattct acatgcaaag 240

cagcagcagc cacgt 255

<210> 412
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 412

anattgtaga ccantanaca tatgtnatat tnggtgatgg ntgtcaaatg gagggantnt 60

caaatgaagc atgctcactt gccggtcact ggggtctagg gaagcttatn gcttnatatg 120

atgacaacca catttccatt gatggggaca ctgagattgc attcactgag aatgttgatc 180

aacgttttga ggcacttggg tggcatgtaa tttgggtgaa gaatggaaat actggatatg 240

atgaaattcg tgcagccatt aaggaagcaa aggctgtcaa agacgaaccc actatgatcc 300

aggtaaccac taccattgga ttggttctcc aaa 333

<210> 413
<211> 260
<212> DNA
<213> Glycine max

<400> 413

aacaagcctg acaatgagat tgttgaccat tacacatatg ttatattggg tgatggttgt 60

caaatggagg gaatttcaaa tgaagcttgc tcacttgccg gtcactgggg tctaggaaag 120

ctcattgctt tatatgatga caatcacatt tccattgatg gtgacactga gattgcattc 180

actgagaatg ttgatcagcg ttttgaagca cttggatggc atgtaatttg ggtgaagaat 240

ggaaatactg gatatgatga 260

<210> 414
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 414

cacttggctg cacgatttaa caatcctgnc antgagattg ttgaccatta nacatatgtt 60

atattgggtg atggttgtca aatggaggga atttcaaatg aagcatgctc acttgccgnc 120

tcactggggt ctagggaagc ttattgcttt ntatgatgac aaccacattt ccattnctgg 180

ggacactgag attgcattca ctgagantgt tgatcaacgt ttgaggcact tgggtggcat 240

gtaatttggg tgaagaatgg anatactgga tatgatgaaa ttcgtgcg 288

<210> 415
<211> 242
<212> DNA
<213> Glycine max

<400> 415

gaatttcaaa tgaagcatgc tcacttgccg gtcactgggg tctagggaag cttattgctt 60

tatatgatga caaccacatt tccattgatg gggacactga gattgcattc actgagaatg 120

ttgatcaacg ttttgaggca cttgggtggc atgtaatttg ggtgaagaat ggaaatactg 180

gatatgatga aattcgtgca gccattaagg aagcaaaggc tgtcaaagac aaacccacta 240

tg 242

<210> 416
<211> 251
<212> DNA
<213> Glycine max

<400> 416

caaatggagg gaatttcaaa tgaagcatgc tcacttgccg gtcactgggg tctagggaag 60

cttattgctt tatatgatga caaccacatt tccattgatg gggacactga gattgcattc 120

actgagaatg tgatcaacgt tttgaggcac ttgagtggca tgtaatttgg gtgaagaatg 180

gaaatactgg atatgatgaa attcgtgcag ccattaagga agcaaaggct gtcaaagaca 240

cccactatga t 251

<210> 417
<211> 245
<212> DNA
<213> Glycine max

<400> 417

gcacgattta acaagcctga caatgagatt gttgaccatt acacatatgt tatattgggt 60

gatggttgtc aaatggaggg aatttcaaat gaagcatgct cacttgccgg tcactggggt 120

ctagggaagc ttattgcttt atatgatgac aaccacattt ccattgatgg ggacactgag 180

attgcattca ctgagaatgt tgatcaacgt tttgaggcac ttgggtggca tgtaatttgg 240

gtgaa 245

<210> 418
<211> 249
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 418

gttgatcang cgttttgnaa gcacttggat ggcatgtaat ttgggtgaag natggaaata 60

ctggatatga tgaaattgcg tgcagccatt aaagaagnaa aggctgtcaa agacaaaccc 120

actttgatca aggtanccac tagnattgga ttaggttctc caaacaaggc taattcncac 180

agtgttcatg ggncgtgcat taggtgctaa agaagtggat gctacnangn anaatnttgg 240

atggcnata 249

<210> 419
<211> 240
<212> DNA
<213> Glycine max

<400> 419

cattgatgca gttgagaagg ccaactctgg tcaccctggt ctccccatgg ggtgtgctct 60

aatgggctca cattctctac gatgagataa tgaggtacaa ttctaagaac cccgcttggt 120

tcaaccgtga cgtttcgttc tctctgctgg acatggctgc atgctccaat atgctctcct 180

tcaccttgct ggctatgaca ctgttcagga acaagacctt aaggaattcc gacaatgggg 240

<210> 420
<211> 283
<212> DNA
<213> Glycine max

<400> 420

caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc 60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa 120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc 180

acttgtggct ttgggttact gttacatgac ttgtttttg agatatcact ttagccacaa 240

taaggaagat tagatgttct gcatatgatt gtcagaggaa cca 283

<210> 421
<211> 259
<212> DNA
<213> Glycine max

<400> 421

caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc 60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa 120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc 180

acttgtggct ttgggttact gttacatgac ttgtttttg agatatcact ttagccacaa 240

taaggaagat tagattgtt 259

<210> 422
<211> 256
<212> DNA
<213> Glycine max

<400> 422

caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc 60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa 120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc 180

acttgtggct ttgggttact gttacatgac ttgtttttg agatatcact ttagccacaa 240

taaggaagat tagatt 256

<210> 423
<211> 271
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 423

aaaggaaagg ccataggcat tgatcgattt ggagcaagtg ctccagctgg aaaaatatac 60

aaggagtttg gtatcaccaa ggaagctgtt attgctgctg ccaaagaact ttcgtaatat 120

atttgttgag tntcttttat ctcatctaga acttgtggtt ttcacttgtg gctttgggtt 180

actgttacat gacttgtttt ttgagatatc actttagcca caatanggaa gatagattgt 240

tcttgcatat gattgtcaga ggaaccactt a 271

<210> 424
<211> 258
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 424

tctgcactgt gtgaagctgg agttatttat gtgatgactc atgattcgat tggacttgga 60

gaggatggac caactcatca gccaatagag catttggcaa gcttcagggc aatgccaaac 120

actttgatgc ttgtccagct gatggnaatg aaactgctgg atcatacaaa gttgctgtgg 180

ttaacaggaa gagaccctca attcttgcac tttctaggca aaagttgacc caacttccag 240

ganttctatt gagggagt 258

<210> 425
<211> 209
<212> DNA
<213> Glycine max

<400> 425

gctgatggta atgaaactgc tggatcatac aaagttgctg tggttaacag gaagagaccc 60

tcaattcttg cactttctag gcaaaagttg acccaacttc caggaacttc tattgaggga 120

gttgaaaagg gtggctacac catttcagac aactcatcag gtaacaagcc tgatgttatt 180

ttgattggaa ctggttctga gttggaaat 209

<210> 426
<211> 257
<212> DNA
<213> Glycine max

<400> 426

cgaccaactc atcagccaat agagcatttg gcaagcttca gggcaatgcc aaacacttag 60

atgcttcgtc cagctgatgg taatgaaact gctggatcat acaaagttgc tgtggttaac 120

aggtagagac cctcaattct tgcactttct aggcaaaagt tgacccaact tccaggaact 180

tctattgagg gatttgaaaa gggtggctac accattctcg aacagctcat caggtaacaa 240

gccggatgtt attttga 257

<210> 427
<211> 246
<212> DNA
<213> Glycine max

<400> 427

gctgtggtta acaggaagag accctcaatt cttgcacttt ctaggcaaaa gttgacccaa 60

cttccaggaa cttctattga gggagttgaa aagggtggct acaccatttc agacaactca 120

tcaggtaaca agcctgatgt tattttgatt ggaactggtt ctgagttgga aattgctgct 180

gctgctgctg aggatctagg aaaggaagga aaagctgtta gagttgtttc ttttgttagc 240

tgggaa 246

<210> 428
<211> 168
<212> DNA
<213> Glycine max

<400> 428

gaccaactca tcagccaata gagcacttgg caagcttcag ggcaatgcca aacactttga 60

tgcttcgtcc agctgatggt aatgaaactg ctggatcata caaagttgct gtggttaaca 120

ggaagagacc ctcaattctt gcactttcta ggcaaaagtt gacccaac 168

<210> 429
<211> 168
<212> DNA
<213> Glycine max

<400> 429

aattcttgca ctttctaggc aaaagttgac ccaacttcca ggaacttcta ttgagggagt 60

tgaaaagggt ggctacacca tttcagacaa ctcatcaggt aacaagcctg atgttatttt 120

gattggaact ggttctgagt tggaaattgc tgctgctgct gctgagga 168

<210> 430
<211> 254
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 430

ctcatgattc gattggactt gggagaggat ggaccaacta catcagccaa tagagcattt 60

ngcaagcttc agggcaatgc caaacacttn cntgcttcgt ccagctatgg taatgaaact 120

gctggatcat acaaagttgc tgtggttaac aggaagagac cctcaattct tgcactttct 180

agncaaaagt tgacccaact tccaggaact tctattggag gtgaaaaggg tggctacacc 240

atttcagana actc 254

<210> 431
<211> 117
<212> DNA
<213> Glycine max

<400> 431

aattcttgca cttgctaggc aaaagttgac ccagcttcca ggaacttcta ttgagggagt 60

tgaaaagggt ggctacacca tttcagacaa ctcatcaggt aacaagcctg atgttat 117

<210> 432
<211> 263
<212> DNA
<213> Glycine max

<400> 432

atgagaggtg ccataaagct ttctgcgctg tctgaggctg gggttattta atgtcatgac 60

ccatgattca ataggacttg gagaagatgg gccaacccac cagcctattg agcacctagc 120

aagcttccgg gcaatgccaa acattttgat gcttcgtccc gccgacggta acgaaacagc 180

cggagcatac aaagtggccg tgctcaacag gaagagaccc tccattcttg ccctatccag 240

gcaaaaactg ccccagcttc ccg 263

<210> 433

<211> 257
<212> DNA
<213> Glycine max

<400> 433

catttgatg cttcgtcctg ccgacggtaa cgaaacagcc ggagcataca aagtggccgt 60

gctcaacagg aagagaccct ccattcttgc cctatccagg caaaaactgc cccagcttcc 120

cggaacttcc attgaaggag ttgaaaaggg tggttacacc atttcggaca actccactgg 180

caacaagcct aatgacattt ggaccggaac tggttcggaa ttggaaatcg ctgccaaagc 240

tgctgatgac ctaagga 257

<210> 434
<211> 253
<212> DNA
<213> Glycine max

<400> 434

tcatgaccca tgattcaata ggacttggag aagatgggcc aacccaccag cctattgagc 60

acctagcaag cttccgggca atgccaaaca ttttgatgct tcgtcccgcc gacggtaacg 120

aaacagccgg agcatacaaa gtggccgtgc tcaacaggaa gagaccctcc attcttgccc 180

tatccaggca aaaactgccc cagcttcccg gaacttccat tgaaggagtt gaaaagggtg 240

gttacaccat ttc 253

<210> 435
<211> 134
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 435

ttggagaaga tgggccaacc caccagccta ttgagcacct agnnagcttc cgggcaatgc 60

caaacatttt gatgcttcgt cccgccgacg gtaacgaaac agccgnagca taccaagtgg 120

ccgtgtcaac aggg 134

<210> 436
<211> 387
<212> DNA
<213> Glycine max

<400> 436

cccacgcgtc cgcccacgcg tccgggtcac aacaaccatt ggttatggtt ctcctaacaa 60

ggctaactcc tacagtgtgc atggaagtgc actgggtgcc aaagaagttg atgccacaag 120

gcagaacctt ggatggtcac atgagccatt ccacgtgcct gaggatgtca aaaagcattg 180

gagtcgccac accccctgagg gtgctgcact tgaagctgaa tggaatgcta agtttgctga 240

gtatgaaaag aaatacaagg aggaagctgc agaattgaaa tctattatca atggtgaatt 300

ccctgctggt tgggagaaag cactttcgac atacactcca gagagcccag cggatgccac 360

cagaaacctg tctcaaacaa accttaa 387

<210> 437
<211> 316
<212> DNA
<213> Glycine max

<400> 437

ggggttattt atgtcatgac ccatgattca ataggacttg gagaagatgg gccaacccac 60

caccctattg agcacctagc aagcttccgg gcaatgccaa acattttgat gcttcgtccc 120

gccgacggta acgaaacagc cggagcatac aaagtggccg tgctcaacag gaagagaccc 180

tccattcttg ccctgtccag gcaaaaactg ccccagcttc ccggaacttc cattgaagga 240

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt 300

ttgatcggaa ctggtt 316

<210> 438
<211> 301
<212> DNA
<213> Zea mays

<400> 438

gtcatcttcc acgtctccaa gaccggcggc cacctcgggt ccagcctcgg cgtggtggag 60

ctcaccgtcg cgctgcacta cgtcttcaac gcgccgcagg accgcatcct ctgggacgtc 120

ggccaccagt cgtacccgca caagatcctg acggggcggc gcgacaagat gccgacgatg 180

cggcagacca acggcctggc gggcttcccc aagcgcgccg agagcgagta cgacagcttc 240

ggcacgggcc acagctccac caccatctcc gcggcgctcg ggatggcggt gggccgggac 300

c 301

<210> 439
<211> 265
<212> DNA
<213> Zea mays

<400> 439

cggtgccgcc caactacaaa ggcactcccc tcgaggtcgg caaaggcagg atcctgcttg 60

agggcgaccg ggtggcgctg ctggggtacg ggtcggcagt gcagtactgc ctgactgccg 120

cgtccctggt gcagcgccac ggcctcaagg tcaccgtcgc cgacgcgagg ttctgcaagc 180

cgctggacca cgccctgatc aggagcctgg ccaagtccca cgaggtgctc atcaccgtgg 240

aggaaggctc catcggcggg ttcgg 265

<210> 440
<211> 245
<212> DNA
<213> Zea mays

<400> 440

gtgggccggg acctcaaggg cggcaagaac aacgtggtcg cggtgatcgg cgacggcgcc 60

atgacggccg ggcaggcgta cgaggccatg aacaacgccg ggtacctgga ctccgacatg 120

atcgtcatcc tcaacgacaa caagcaggtg tccttgccca cggcgacgct cgacgggccg 180

gtgccgcccg taggcgcgct cagcagcgac ctcagcaagc tgcagtcaag caggccgctc 240

aagga 245

<210> 441
<211> 156
<212> DNA
<213> Zea mays

<400> 441

gaagcaggtc ggtggctcag tgcacgagct ggcggcgaag gtggacgagt acgcccgcgt 60

catgatcagc gggcccggct cctcgctctt cgaggagctc ggtctctact acatcggccc 120

cgtcgacggc cacaacatcg acgacctcat caccat 156

<210> 442
<211> 271
<212> DNA
<213> Zea mays

<400> 442

gtgtacgtga cggtagccga cgcccggttc tgcaagccgc tggacacggc gctgatccgg 60

gagctcgccg ccgagcacga ggtgctgatc accgccgagg agggatccat cggcgggttc 120

ggctcccacg tcgcacacta cctcagcctg accggcctcc tggacgggcc cctcaaactg 180

agatccatgt tcctgccgga ccggtacatc gaccatggcg caccgcagga ccagatcgag 240

gattcagggc tgacgccgcg gcacatcgcc g 271

<210> 443
<211> 288
<212> DNA
<213> Zea mays

<400> 443

ccgacgcccg gttctgcaag ccgctggaca cggcgctgat ccgggagctc gccgccgagc 60

acgaggtgct gatcaccgcc gaggagggat ccatcggcgg gttcggctcc cacgtcgccc 120

actacctcag cctgaccggc ctcctggacg ggcccctcaa actgagatcc atgttcctgc 180

cggaccggta catcgaccat ggcgcaccgc aggaccagat cgatgaggca gggctgacgc 240

gcggcacatc gccgccaccg tgctgtccct gctggggagg ccattgga 288

<210> 444
<211> 340
<212> DNA
<213> Zea mays

<400> 444

aagagcacca agaccaccgg ccccgtcctc atccacgtcg tcaccgagaa gggccgcggc 60

taccccctacg ccgagcgagc cgccgacaag taccacggtg tcgccaagtt tgatccggcg 120

accgggaagc agttcaagtc ccccgccaag acgctgtcct acaccaacta cttcgccgag 180

gcgctcatcg ccgaggcggg ccaggacagc aagatcgtgg ccatccacgc ggccatgggc 240

ggcggcacgg ggctcaacta cttcctccgc cgcttcccga accggtgctt cgacgtcggg 300

atcgcggaca gcacgccgtc acgttcgggc cggctggctg 340

<210> 445
<211> 245
<212> DNA
<213> Zea mays

<400> 445

gtaccacggt gtcgccaagt ttgatccggc gaccgggaag cagttcaagt cccccgccaa 60

gacgctgtcc tacaccaact acttcgccga ggcgctcatc gccgaggcgg agcaggacag 120

caagatcgtg gccatccacg cggccatggg cggcggcacg ggctcaact acttcctccg 180

ccgcttcccg agccggtgct tcgacgtcgg gatcgcggag cagcacgccg tcacgttcgc 240

ggccg 245

<210> 446
<211> 298
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 446

cgatctgcag aagctaccgg taaggttcgt catggacagg gccgggctgg tcggcgcgga 60

cgggccgacc cactgcgggg cgttcgacgt cgcgtacatg gcctgcctgc ccaacatggt 120

cgtcatggcc ccgtccgacg aggccgagct ctgccacatg gtcgccaccg ccgcggcaat 180

cgacgaccgc ccgtcctgct tccgctaccc gagaggcaac ggcgttggcg tcccgttgcc 240

gnccaactac aaaggcactc ccctcgaggt cgggcaaagc aggatcctgc tggagggc 298

<210> 447
<211> 333
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 447

cagggccggg ctggtcggcg cggacgggcc gacccactgc ggggcgttcg acgtcgcgtg 60

catggcctgc ctgcccaaca tggtcgtcat ggccccgtcc gacgaggccg agctctgcca 120

catggtcgcc accgccgcgg caatcgacga ccgcccgtcc tgcttccgct acccgagagg 180

caacggcgtt ggcgtcccgt tgccgcccaa ctacaaaggc actcccctcg aggtcggcaa 240

aggcaggatc ctgctggagg gcgacaccgg ggngctgctg gngtacgggt cgggagtgca 300

gnactggctg accgtcgcgt acctggtgca gcg 333

<210> 448
<211> 240
<212> DNA
<213> Glycine max

<400> 448

caacaagcag gtttctttac caactgctac tcttgatgga cccataccac ctgtaggagc 60

cttgagtagc gctctcagta gattacaatc aaataggcct cttagagaat tgagagaggt 120

tgccaaggga gttcctaaac gaattggagg tcctatgcat gaattggctg caaaagttga 180

cgagtatgct cgtggcatga tcagtggttc tggatcatca ctttttgaag agcttggact 240

<210> 449
<211> 309
<212> DNA
<213> Glycine max

<400> 449

aatgcagggt accttgactc taacatgata attatactta atgacaacaa gcaagtttct 60

ttgcctactg ctactattga tggtcctgca actccaattg gagcccgcaa tagtgcctta 120

agcaaaattc aagcaagcac caaataccgc aaactgagag aagctgcgaa aggcatcaca 180

aagcagatag gaggaacaac acacaacttg cagcaaaggt agatgagtat gcaagaggta 240

tgatcagtgg ttctagtact acacttgttg aggagctcgg cttatactac atatgccctg 300

tggatggtc 309

<210> 450
<211> 233
<212> DNA
<213> Glycine max

<400> 450

aaaacaactg gtcctgtgct gctccatgtt gtcactgaaa aaggccatgg atatccatat 60

gcagaaagag cagcagatta gtaccatgga gttactaagt ttgatccatt aactggaaaa 120

caattcaaat tcaatgctgc cacccagtta tacacaacat actttgcaga ggctttaatt 180

tctgaagcgg aagcttacaa agacattgtc ggaatccatg ctgcaatggg agg 233

<210> 451
<211> 268
<212> DNA
<213> Glycine max

<400> 451

tgtgattctg tatgatagcc gtcactcttt acttccaaaa attgaggagg gcccaaagac 60

atttgtcaat gccctatcta gtaccctgag caagctccag tccagtaaat ctttccggag 120

atttagagaa gctgctaggg gtgttacgaa acgaattggt aggtctgcat gaattggcag 180

ctaaagtgga tgaatatgct cgtggtatga tgggtcctct aggtgctact ctttttgaag 240

agcttgggtt gtactacata ggcccagt 268

<210> 452
<211> 162
<212> DNA
<213> Glycine max

<400> 452

cttccttgtt ggaacatcat ggcttgcgcg caacagtggc tgatgcacgt ttctgcaagc 60

cattggaccg ttctcttatt cttagccttg cccaatcgca cgaggttttg atcactgtgg 120

aagaagggca ataggaggat tcggatctca tgttgttcag tt 162

<210> 453
<211> 232
<212> DNA
<213> Glycine max

<400> 453

gatctctccg ctctctcatc ataccgcact ctcgggtagt tacttcctct tccctctcac 60

tctcaatggg gtctccattt cctcgcccac gctcaccgcc tccaccagat gaagaaaagg 120

ccatgtgggg tatatgcatc cctctccgag agtggagagt attattccca ccgaccgcca 180

actcccctac tagacaccgt caactatcct attcatatga agaatctctc tg 232

<210> 454
<211> 280

<212> DNA
<213> Zea mays

<400> 454

gtgcaccgac caagaaaacc tcgcttcacg atctctacga gctccagggc ctctccccgt 60

ggtatgacaa cctctgccga cctgtcaccg acttgctgcc ccttatcgcc agctgtgttc 120

gtggagtcac cagcaaccct gcagtaatcc tccgtttcca ccttttgttt cttcgcttgc 180

atggttgctg cgcattcact cctgaccgtg tcctcgacgc aatgcagatt ttccagaagg 240

ccatctcatc ctccagcgca tatgatgatc agttcaagca 280

<210> 455
<211> 274
<212> DNA
<213> Zea mays

<400> 455

tgacactcaa ggaactgttg aggaggcaaa gtggttacac aaagtggtca accgccccaa 60

tgtctacata aagatccctg ctaccgcaga atgtgttcat tccatccgtg aagttatcgc 120

taatggcatt agcgtcaacg tcacgcttat attctctatt gcgagatacg aggctgtgat 180

tgatgcttac cttgatgggc tagaggcttc tggcttgagc gacttatctc gagttaccag 240

tgtcgcatcc ttctttgtca gtcgagtcga cacc 274

<210> 456
<211> 306
<212> DNA
<213> Zea mays

<400> 456

ccaacgagca aacccccccat ttgccaccaa ccccgacgag cggcgatgac cggcacgtgt 60

ctaagctggc ggcgccccgt ccggcggcac cgccgctccg gccggcgtcc ctccgcaccg 120

ccgccctcgc cttcgccccc tccgcgcgcc gggtccgcgt ctccgtcgcc gggcgagcca 180

ggagccccat cattgcgatg gcttcggcca aggaaggaaa tggtgcaccg accaagagga 240

ctgcgcttca tgatctctac gagctccagg gcctgtcccc gtggtacgac aacctatgcc 300

gccctg 306

<210> 457
<211> 330
<212> DNA
<213> Zea mays

<400> 457

ccaaggtggg aggcgttggc caagaaaggt gccaagaaac aaaggttgtt gtgggcatcc 60

accggtgtca agaacccagc ttatcctgac actctttatg tggacagtct catcggacct 120

gacacggtca acacgatgcc cgaccaagct ttgcaagcat tcatagacca cggcaccgtt 180

tcaaggacag ttgatgcgaa cgtgtctgag gcggaaggtg tatacagtgc cttggagaag 240

cttggcatcg actgggaaga ggttggaaag cagcttgagc tggaaggcgt ggactccttc 300

aagaagagct ttgacagcct actcgtgagc 330

<210> 458
<211> 317
<212> DNA
<213> Zea mays

<400> 458

gaaattctct ggcccgaggt gggaggcgtt ggccaagaaa ggtgccaaga aacagaggtt 60

gttgtgggca tccaccggtg tcaagaaccc agcttatccc gacactcttt acatcgacag 120

tctcattgga cctgacacgg tcaacacgat gcccgaccaa gctttgcacg cattcataga 180

ccacggcact gtctcgagga cagttgatgc gaatgtgtcc gaggcggaag gtgtatacag 240

cgccttggag aagcttggca ttgactgggg cgaggtcgga aagcagcttg agctggaagg 300

tgtggactcc ttcaaga 317

<210> 459
<211> 306
<212> DNA
<213> Zea mays

<400> 459

cgggaggcgt tggccaagaa aggtgccaag aaacaaaggt tgttgtgggc atccaccggt 60

gtcaagaacc cagcttatcc tgacactctt tatgtggaca gtctcatcgg acctgacacg 120

gtcaacacga tgcccgacca agctttgcaa gcattcatag accacggcac cgtttcaagg 180

acagttgatg cgaatgtgtc tgaggcggaa ggtgtataca gcgccttgga gaagcttggc 240

atcgactggg aagaggttgg aaagcagctt gagctggaga gcgtggactc cttcaagaag 300

agcttt 306

<210> 460
<211> 299
<212> DNA
<213> Zea mays

<400> 460

cttgagcgac ttatctcgag ttaccagtgt cgcatccttc tttgtcagtc gagtcgacac 60

ccttatcgac aaaatgcttg agaagattgg aacacctgag gcacttgcct tgagagggaa 120

ggctgccgtc gcacaggcca aactagcaaa tcggctctac cagaagaaat tctctggccc 180

gaagtgggag gcgttggcca agaaaggtgc caagaaacag aggttgttgt gggcgtccac 240

cggtgtcaag aacccagctt atcccgacac tctttacatc gacagtctca ttggacctg 299

<210> 461
<211> 282
<212> DNA
<213> Zea mays

<400> 461

agcaaatcgg ctctaccaga agaaattctc tggcccaagg tgggaggcgt tggccaagaa 60

aggtgccaag aaacaaaggt tgttgtgggc atccaccggt gtcaagaacc cagcttatcc 120

tgacactctt tatgtggaca gtctcatcgg acctgacacg gtcaacacga tgcccgacca 180

agctttgcaa gcattcatag accacggcac cgtttcaagg acagttgatg cgaacgtgtc 240

tgaggcggaa ggtgtataca gtgccttgga gaagcttggc at 282

<210> 462
<211> 295
<212> DNA
<213> Zea mays

<400> 462

gcgacttatc tcgagttacc agtgtcgcat ccttctttgt cagccgagtc gacaccctta 60

tcgacaaaat gcttgagaag attggaacac ctgaggcact tgccttgaga gggaaggctg 120

ccgtcgcaca ggccaaacta gcaaatcggc tctaccagaa gaaattctct ggcccgaggt 180

gggaggcgtt ggccaagaaa ggtgccaaga aacagaggtt gttgtgggca tccaccggtg 240

tcaagaaccc agcttatccc gacactcttt acatcgacag tctcattgga cctga 295

<210> 463
<211> 313
<212> DNA
<213> Zea mays

<400> 463

tgaatgtgtt ccttccatcc aggaagttat cgctaatggc attagcgtca acgtcacgct 60

tattttctca attgcgagat atgaggctgt gattgatgct tacctcgatg ggctagaggc 120

ttctggactt gagtgactta tcccgagtta ctagcgttgc atccttcttt gtcagccgag 180

tggacaccct tattgacaaa atgcttgaca agattggaac acctgaggcc cttgccttga 240

gaggaaaggc tgcagtagcg caggccaaac tagcaaatcg gctctaccag aagaaattct 300

ctggcccaag gtg 313

<210> 464
<211> 275
<212> DNA
<213> Zea mays

<400> 464

gaacacctga ggcccttgcc ttgagaggaa aggctgcagt agcacaggcc aaactagcaa 60

atcggctcta ccagaagaaa ttctctggcc caaggtggga ggcgttggcc aagaaaggtg 120

ccaagaaaca aaggttgttg tgggcatcca ccggtgtcaa gaacccagct tatcctgaca 180

ctctttatgt ggacagtctc atcggacctg acacggtcaa cacgatgccc gaccaagctt 240

tgcaagcatt catagaccac ggcaccgttt caagg 275

<210> 465
<211> 286
<212> DNA
<213> Zea mays

<400> 465

cccacgcgtc cgcccacgcg tccggtgatt gatgcttacc ttgatgggct agaggcttct 60

ggcttgagcg acttatctcg agttaccagt gtcgcatcct tctttgtcag ccgagtcgac 120

acccttatcg acaaaatgct tgagaagatt ggaacacctg aggcacttgc cttgagaggg 180

aaggctgccg tcgcacaggc caaactagca aatcggctct accagaagaa attctctggc 240

ccgaggtggg aggcgttggc caagaaaggt gccaagaaac agaggt 286

<210> 466
<211> 284
<212> DNA
<213> Zea mays

<400> 466

ctcaaggaac tgttgaagcg gcaaagtggt tacacaaagt ggtcaaccgc cccaatgtct 60

acataaagat cccagctact gcagaatgtg ttccttccat ccaggaagtt atcgctaatg 120

gcattagcgt caacgtcacg cttattttct caattgcgag atatgaggct gtgattgatg 180

cttacctcga tgggctagag gcttctggct tgagtgactt atcccgagtt actagcgttg 240

catccttctt tgtcagccga gtggacaccc ttattgacaa aatg 284

<210> 467
<211> 277
<212> DNA
<213> Zea mays

<400> 467

aaccgcccca atgtctacat aaagatccct gctaccgccg aatgtgttcc ttccatccgg 60

gaagttatcg ctaatggcat tagcgtcaac gtcacgctta ttttctctat tgcgagatac 120

gaggctgtga ttgatgctta ccttgatggg ctagaggctt ctggcttgag cgacttatct 180

cgagttacca gtgtcgcatc cttctttgtc agccgagtcg acacccttat cgacaaaatg 240

cttgagaaga ttggaacacc tgaggcactt gccttga 277

<210> 468
<211> 279
<212> DNA
<213> Zea mays

<400> 468

ttttgagcct atctacgatg agaccgatgg ggctgatggg tatgtctccg tggaggtgtc 60

tcctaggttg gcaaatgaca ctcaaggaac tgttgaggcc gcaaagtggt tacacaaagt 120

ggtcaaccgc cccaatgtct acataaagat ccctgctacc gccgaatgtg ttccttccat 180

ccgggaagtt atcgctaatg gcattagcgt caacgtcacg cttattttct ctattgcgag 240

atacgaggct gtgattgatg cttaccttga tgggctaga 279

<210> 469
<211> 334
<212> DNA
<213> Zea mays

<400> 469

cggacgcgtg ggtccagcgc atatgatgat cagttcaagc agctcatttc ggctggaaag 60

gacgcggaga gcgcttactg ggaactcgtt ataaaggata tccaagatgc gtgcaaactt 120

tttgagccca tctacgatga gactgatggg gctgatgggt atgtctccgt agaggtgtct 180

cctaggttgg caaatgacac tcaaggaact gttgaagcgg caaagtggtt acacaaagtg 240

gtcaaccgcc ccaatgtcta cataaagatc ccagctactg cagaatgtgt tccttccatc 300

caggaagtta tcgctaatgg cattagcgtc aacg 334

<210> 470
<211> 322
<212> DNA
<213> Zea mays

<400> 470

tagcagctca tttcggcagg aaaggatgcg gagagcgctt actgggaact cgttataaag 60

gatatccaag atgcgtgcaa actttttgag cccatctacg acgagactga tggggctgat 120

gggtatgtct ccgtagaggt gtctcctagg ttggcaaatg acactcaagg aactgttgaa 180

gcggcaaagt ggttacacaa agtggtcaac cgccccaatg tctacataaa gatcccagct 240

actgcagaat gtgttccttc catccaggaa gttatcgcta atggcattag cgtcaacgtc 300

acgcttattt tctcaattgc ga 322

<210> 471
<211> 283
<212> DNA
<213> Zea mays

<400> 471

gttgttgtgg gcatccaccg gtgtcaagaa cccagcttat cccgacactc tttacatcga 60

cagtctcatt ggacctgaca cggtcaacac gatgcccgac caagctttgc acgcattcat 120

agaccacggc actgtctcga ggacagttga tgcgaatgtg tccgaggcgg aaggtgtata 180

cagcgccttg gagaagcttg gcattgactg gggcgaggtc ggaaagcagc ttgagctgga 240

aggtgtggac tccttcaaga agagctttga cagcctactc gtg 283

<210> 472
<211> 265
<212> DNA
<213> Zea mays

<400> 472

gccttatcga caaaatgctt gagaagattg gaacacctga ggcacttgcc ttgagaggga 60

aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa ttctctggcc 120

cgaggtggga ggcgttggcc aagaaaggtg ccaagaaaca gaggttgttg tgggcatcca 180

ccggtgtcaa gaacccagct tatcccgaca ctctttacat cgacagtctc attggacctg 240

acacggtcaa cacgatgccc gacca 265

<210> 473
<211> 240
<212> DNA
<213> Zea mays

<400> 473

caagattgga acacctgagg cccttgcctt gagaggaaag gctgcagtag cacaggccaa 60

actagcaaat cggctctacc agaagaaatt ctctggccca aggtgggagg cgttggccaa 120

gaaaggtgcc aagaaacaaa ggttgttgtg ggcatccacc ggtgtcagga acccagctta 180

tcctgacact ctttatgtgg acagtctcat cggacctgac acggtcaaca cgatgcccga 240

<210> 474
<211> 301
<212> DNA
<213> Zea mays

<400> 474

ccgacaaggt ccgggacgcg tggctgggaa ctcgttataa aggatatcca agatgcgtgc 60

aaactttttg agcccatata cgatgagact gatagggctg atgggtatgt ctccgtagag 120

gtgtctccta ggttggcaaa tgacactcaa ggaactgttg aagcggcaaa gtggttacac 180

aaagtggtca accgccccaa tgtctacata aagatcccag ctactgcaga atgtgttcct 240

tccatccagg aagttatcgc taatggcatt agcgtcaacg tcacgcttat tttctcaatt 300

g 301

<210> 475
<211> 300
<212> DNA
<213> Zea mays

<400> 475

agaggcttct ggcttgagcg acttatctcg agttaccagt gtcgcatcct tctttgtcag 60

ccgagtcgac acccttatcg acaaaatgct tgagaagatt ggaacacctg aggcacttgc 120

cttgagaggg aaggctgccg tcgcacaggc caaactagca aatcggctct accagaagaa 180

attctctggc ccgaggtggg aggcgttggc caagaaaggt gccaagaaac agaggttgtt 240

gtgggcatcc accggtgtca agaacccagc ttatcccgac actctttaca tcgacagtct 300

<210> 476
<211> 267
<212> DNA
<213> Zea mays

<400> 476

ggcaaatgac actcaaggaa ctgttgaagc ggcaaagtgg ttacacaaag tggtcaaccg 60

ccccaatgtc tacataaaga tcccagctac tgcagaatgt gttccttcca tccaggaagt 120

tatcgctaat ggcattagcg tcaacgtcac gcttattttc tcaattgcaa gatatgaggc 180

tgtgattgat gcttacctcg atgggctaga ggcttctggc ttgagtgact tatcccgagt 240

tactagcgtt gcatccttct ttgtcag 267

<210> 477
<211> 293
<212> DNA
<213> Zea mays

<400> 477

cccacgcgtc cgcccacgcg tccgggaact cgttataaag gatatccaag atgcgtgcaa 60

actttttgag cccatctacg acgagactga tggggctgat gggtatgtct ccgtagaggt 120

gtctcctagg ttggcaaatg acactcaagg aactgttgaa gcggcaaagt ggttacacaa 180

agtggtcaac cgccccaatg tctacataaa gatcccagct actgcagaat gtgttccttc 240

catccaggaa gttatcgcta atggcattag cgtcaacgtc acgcttttct caa 293

<210> 478
<211> 257
<212> DNA
<213> Zea mays

<400> 478

gcgttggcca agaaaggtgc caagaaacag aggttgttgt gggcatccac cggtgtcaag 60

aacccagctt atcgcgacac tctttacatc gacagtctca ttggacctga cacggtcaac 120

acgatgcccg accaagcttt gcacgcattc atagaccacg gcactgtctc gaggacagtt 180

gatgcgaatg tgtccgaggc ggaaggtgta tacagcgcct tggagaagct tggcattgac 240

tggggcgagg tcggaaa 257

<210> 479
<211> 229
<212> DNA
<213> Zea mays

<400> 479

cccttatcga caaaatgctt gagaagattg gaacacctga ggcacttgcc ttgagaggga 60

aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa ttctctggcc 120

cgaggtggga ggcgttggcc aagaaaggtg ccaagaaaca gaggttgttg tgggcgtcca 180

ccggtgtcaa gaacccagct tatcccgaca ctctttacat cgacagtct 229

<210> 480
<211> 263
<212> DNA
<213> Zea mays

<400> 480

atggggctga tgggtatgtc tccgtagagg tgtctcctag gttggcaaat gacactcaag 60

gaactgttga agcggcaaag tggttacaca aagtggtcaa ccgccccaat gtctacataa 120

agatcccagc tactgcagaa tgtgttcctt ccatccagga agttatcgct aatggcatta 180

gcgtcaacgt cacgcttatt ttctcaattg caagatatga ggctgtgatt gatgcttacc 240

tcgatgggct agaggcttct ggc 263

<210> 481
<211> 300
<212> DNA
<213> Zea mays

<400> 481

gccaaggaag gaagcggtgc accgaccaag aggactgcgc ttcatgatct ctacgagctc 60

cagggcctgt ccccgtggta cgacaaccta tgccgccctg tcacagactt gctgcccatt 120

atcgccagcg ggtccgtgga gtcaccagca acccaacgat tttccaaaag gccatttcat 180

cgtccagcgc atatgatgat cagttcaagc agctcatttc ggcaggaaag gatgcggaga 240

gcgcttactg ggaactcgtt ataaaggata tccaagatgc gtgcaaactt tttgagccca 300

<210> 482
<211> 312
<212> DNA
<213> Zea mays

<400> 482

tccaaccaag ggttcggaaa gtcaaggcta atttccccaa tgtgggaaac cgaggctggg 60

attgaggcta accttaatgg gcaaaaggct tctggcttga gcgacttatc tcgagttacc 120

agtgtcgcat ccttctttgt cagtcgagtc gacaccctta tcgacaaaat gcttgagaag 180

attggaacac ctgaggcact tgccttgaga gggaaggctg ccgtcgcaca ggccaaacta 240

gcaaatcggc tctaccagaa gaaattctct ggcccgaggt gggaggcgtt ggccaagaaa 300

ggtgccaaga aa 312

<210> 483
<211> 264
<212> DNA
<213> Zea mays

<400> 483

gcaacccaac gattttccaa aaggccattt catcgtccag cgcatatgat gatcagttca 60

agcagctcat ttcggcagga aaggatgcgg agagcgctta ctgggaactc gttataaagg 120

atatccaaga tgcgtgcaaa ctttttgagc ccatctacga cgagactgat ggggctgatg 180

ggtatgtctc cgtagaggtg tctcctaggt tggcaaatga cactcaagga actgttgaag 240

cggcaaagtg gttacacaaa gtgg 264

<210> 484
<211> 232
<212> DNA
<213> Zea mays

<400> 484

ggtcaacacg atgcccgacc aagctttgca ggcattcata gaccacggca ctgtttcgag 60

gacagttgat gcgaatgtgt ccgaggcgga aggtgtatac agcgccttgg agaagcttgg 120

cattgactgg ggcgaggtcg gaaagcagct tgagctggaa ggtgtggact ccttcaagaa 180

gagctttgac agcctactcg tgagcctgca ggagaagggc aactagcctc aa 232

<210> 485
<211> 258
<212> DNA
<213> Zea mays

<400> 485

caaacttttt gagcccatct acgacgagac tgatggggct gatgggtatg tctccgtaga 60

ggtgtctcct aggttggcaa atgacactca aggaactgtt gaagcggcaa agtggttaca 120

caaagtggtc aaccgcccca atgtctacat aaagatccca gctactgcag aatgtgttcc 180

ttccatccag gaagttatcg ctaatggcat tagcgtcaac gtcacgctta ttttctcaat 240

tgcgagatat gaggctgt 258

<210> 486
<211> 328
<212> DNA
<213> Zea mays

<400> 486

aaagtggtta cacaaagtgg tcaaccgccc caatgtctac ataaagatcc ctgctaccgc 60

cgaatgtgtt cattccatcc gtgaagttat cgctaatggc attagcgtca acgtcacgct 120

tattttctct attgcgagat acgaggctgt gattgatgct taccttgatg ggctagaggc 180

ttctggcttg agcgacttat ctcgagttac cagtgtcgca tccttctttg tcagtcgagt 240

cgacaccctt atcgacaaaa tgttgagaag atggaacacc tgaggcattg ccttgagagg 300

gaaggtgccg tcgcacagcc aactagca 328

<210> 487
<211> 274
<212> DNA
<213> Zea mays

<400> 487

cccacgcgtc cggtcaccga cttgctgccc cttatcgcca gcggtgttcg tggagtcacc 60

agcaaccctg caattttcca gaaggccatc tcatcctcca gcgcatatga tgatcagttc 120

aagcagctca tttcgggcgg aaaggacgcg gagagcgctt actgggaact tgttataaag 180

gatatccaag acgcgtgcag tctttttgag cctatctacg atgagaccga tggggctgat 240

gggtatgtct ccgtggaggt gtctcctagg ttgg 274

<210> 488
<211> 213
<212> DNA
<213> Zea mays

<400> 488

cggacggtgg gcgacaaaat gcttgagaag attggaacac ctgaggcact tgccttgaga 60

gggaaggctg agcgtcgcac aggccaaact agcaaatcgg ctctaccaga agaaattctc 120

tggcccgagg tgggaggcgt tggccaagaa aggtgccaag aaacagaggt tgttgtgggc 180

gtccaccggt gtcaagaacc cagcttatcc cga 213

<210> 489
<211> 262
<212> DNA
<213> Zea mays

<400> 489

tttcatcgtc cagcgcatat gatgatcagt tcaagcagct catttcggct ggaaaggacg 60

cggagagcgc ttactgggaa ctcgttataa aggatatcca agatgcgtgc aaactttttg 120

agcccatcta cgatgagact gatggggctg atgggtatgt ctccgtagag gtgtctccta 180

ggttggcaaa tgacactcaa ggaactgttg aagcggcaaa gtggttacac aaagtggtca 240

accgccccaa tgtctacata aa 262

<210> 490
<211> 252
<212> DNA
<213> Zea mays

<400> 490

cgatggggct gatgggtatg tctccgtgga ggtgtctcct aggttggcaa atgacactca 60

aggaactgtt gaggcggcaa agtggttaca caaagtggtc aaccgcccca atgtctacat 120

aaagatccct gctaccgccg aatgtgttcc ttccatccgg gaagttatcg ctaatggcat 180

tagcgtcaac gtcacgctta ttttctctat tgcgacatac gaggctgtga ttgatgctta 240

ccttgatggg ct 252

<210> 491
<211> 239
<212> DNA
<213> Zea mays

<400> 491

cagcaaccca acgattttcc aaaaggccat ttcatcgtcc agcgcatatg atgatcagtt 60

caagcagctc atttcggctg gaaaggacgc ggagagcgct tactgggaac tcgttataaa 120

ggatatccaa gatgcgtgca aactttttga gcccatctac gatgagactg atggggctga 180

tgggtatgtc tccgtagagg tgtctcctag gttggcaaat gacactcaag gaactgttg 239

<210> 492
<211> 196
<212> DNA
<213> Zea mays

<400> 492

gaaaggtgcc aagaaacaaa ggttgttgtg ggcatccacc ggtgtcaaga acccagctta 60

tcctgacact ctttatgtgg acagtctcat cggacctgac acggtcaaca cgatgcccga 120

ccaagctttg caagcattca tagaccacgg caccgtttca aggacagttg atgcgaacgt 180

gtctgaggcg gaaggt 196

<210> 493
<211> 355
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 493

atctctacga gctccagggc ctgtcaccgt ggtacgacaa cctatgccgc cctgtcacag 60

acttgctgcc cattatcgcc agcgaggtcc gtggagtcac cagcaatcca acgattttcc 120

anaaggccat ttcatcgtcc agcgcatatg atgatcagtt caagcagctc atttcggctg 180

gaaaggacgc ggagagcgct tactgggaac tcgttataaa ggatatccaa gatgcgtgca 240

aactttttga gcccatctac gatgagactg atggggctga tgggtatgtc tccgtagagg 300

tgtctcctag gttggcaaat gacactcaag gaactgttga agcggcatag tggtt 355

<210> 494
<211> 270
<212> DNA
<213> Zea mays

<400> 494

gactagttct agatcgccag cggcgtccgt ggagtcacca gcaacccaac gattttccaa 60

aaggccattt catcgtccag cgcatatgat gatcagttca agcagctcat ttcggcagga 120

aaggatgcgg agagcgctta ctgggaactc gttataaagg atatccaaga tgcgtgcaaa 180

ctttttgagc ccatctacga cgagactgat ggggctgatg ggtatgtctc cgtagaggtg 240

tctcctaggt tggcaaatga cactcaagga 270

<210> 495
<211> 226
<212> DNA
<213> Zea mays

<400> 495

gacgcggaga gcgcttactg ggaactcgtt ataaaggata tccaagatgc gtgcaaactt 60

tttgagccca tctacgatga gactgatggg gctgatgggt atgtctccgt agaggtgtct 120

cctaggttgg caaatgacac tcaaggaact gttgaagcgg caaagtggtt acacaaagtg 180

gtcaaccgcc ccaatgtcta cataaagatc ccagctactg cagaat 226

<210> 496
<211> 234
<212> DNA
<213> Zea mays

<400> 496

cccacgcgtc cgcccacgcg tccgggaaag gatgcggaga gcgcttactg ggaactcgtt 60

ataaaggata tccaagatgc gtgcaaactt tttgagccca tctacgacga gactgatggg 120

gctgatgggt atgtctccgt agaggtgtct cctaggttgg caaatgacac tcaaggaact 180

gttgaagcgg caaagtggtt acacaaagtg gtcaaccgcc ccaatgtcta cata 234

<210> 497
<211> 313
<212> DNA
<213> Zea mays

<400> 497

ccgagtccgc gtttccgtcg ccgggcgagc caggagcccc atcattgcga tggcttcggc 60

caaggaagga agcggtgcac cgaccaagag gactgcgctt catgatctct acgagctcca 120

gggcctgtcc ccgtggtacg acaacctatg ccgccctgtc acagacttgc tgcccattat 180

cgccagcggc gtccgtggag tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc 240

gtccagcgca tatgatgatc agttcaagca gctcatttcg gcaggaaagg atgcggagag 300

cgcttactgg gaa 313

<210> 498
<211> 243
<212> DNA
<213> Zea mays

<400> 498

ggatatgcaa gatgcgtgca aactttttga gcccatctat gacgagactg atggggctga 60

tgggtatgtc tccgtagagg ggtctcctag gttggctaat gacactcaat gtactgttga 120

agctgcaaag tggttacaca aagttgtcaa ccgccccaat gtctacataa agatcccagc 180

tactgcagaa tgtgttcctt ccatccagga agttatccct aatggcatta gcgtcaacgt 240

cac 243

<210> 499
<211> 281
<212> DNA
<213> Zea mays

<400> 499

cacgcttatt ttctctattg cgacatacga ggctgtgatt gatgcttacc ttgatgggct 60

agaagcttcg ggcttgagcg acttatctcg agttaccagt gtcgcatcct tctttgtcag 120

ccgagtcgac acccttatcg acaaaatgct gaaaatattg gaacacctga ggcacttgcc 180

ttgagaggga aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa 240

ttctctggcc caaggtggga ggcgttggcc aagaaaggtg c 281

<210> 500
<211> 320
<212> DNA
<213> Zea mays

<400> 500

gtctcgagga cagttccgtg gtctatgaat gcgtgcaaag cttggtcggg catcgtgttg 60

accacggcac tgtctcgagg acagttgatg cgaatgtgtc cgatgcggaa cgtgtataca 120

gcgccttgga gaatcttggc attgactggg gcgatgtcgg aaagcagctt gagctggaag 180

gtgtggactc cttcaagaag agctttgaca gcctactcgt gagcctacag gagaatggca 240

acagcctcaa gacggcaact gtgtaaaact gagaagattg ggtagcggcg ggtgaacgat 300

tttactatat aaaatgctag 320

<210> 501
<211> 318
<212> DNA
<213> Zea mays

<400> 501

tgttggccaa gcaagagtgc caacgaaaca gcacgttcgc tgtagcgcat cccttggtgt 60

ccagaaccca gcttgtcccg cgactaccta catcgacagt ctcattgggc ctgacacggt 120

caacacgatg cccgaccaag ctttgcacgc attcatagac cacggcactg tctcgaggac 180

agttgatgcg aatgtgtccg aggcggaagg tgtatacagc gccttggaga agcttggcat 240

tgactcgggc gaggtcggaa agcagcttga gctggaaggt gtggactctt caagcagact 300

ttgacagcct actcgtga 318

<210> 502
<211> 283
<212> DNA
<213> Zea mays

<400> 502

cagacgcgtg gggtccgcgt ctccgtcgcc gggcgagcca ggagccccat cattgcgatg 60

gcttcggcca aggacggaaa tggtgcaccg accaagagga ctgcgcttca tgatctctac 120

gagctccagg gcctgtcccc gtggtacgac aacctatgcc gccctgtcac agacttgctg 180

cccattatcg ccagcggcgt ccgtggagtc accagcaacc caacgatttt ccaaaaggcc 240

atttcatcgt ccagcgcata tgatgatcag ttcaagcagc tca 283

<210> 503
<211> 275
<212> DNA
<213> Zea mays

<400> 503

atctcatcct ccagcgcata tgatggttat ctggaccatt gcagggttgc tggtgactcc 60

acgaacaccg ctattttcca gaaggtcatc tcatcctcca gcgcatatga tgatcagttc 120

aagcagctca tttcgggcgg aaatgacgcg gagagtgctt actgcgaact tgttatacag 180

gatatccaag acgcgtgcag tctttttgag cctatctacg atgagaccga tggggctgat 240

gggtatgtct ccgtggaggt gtctcctagg ttggc 275

<210> 504
<211> 184
<212> DNA
<213> Zea mays

<400> 504

accagcaacc ctacaatttt ccagaaggcc atctcatcct ccagcgcata tgatgatcag 60

ttcaagcagc tcatttcggg cggaaaggac gcggagagcg cttactggga actcgttata 120

aaggatatcc aagacgcgtg cagtcttttt gagcctatct acgatgagac cgatggggct 180

gatg 184

<210> 505
<211> 262
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 505

cccacgcgtc cgatgtgtct gaggcggaag gtgtatacag cgccttggag aagcttggca 60

tcgactggga agaggttgga aagcagcttg agctggaagg cgtggactcc ttcaagaaga 120

gctttgacag cctactcgtg agcctgcagg agaagggcaa cagcctcaag atggcgagtg 180

tgtaaagctg agaagattgg gtacctgcga gtgaacgatt ttactanata naatgctagc 240

ttgctggctc tcctcttagt tt 262

<210> 506
<211> 291
<212> DNA
<213> Zea mays

<400> 506

cggctcgagg tttcaaggac agttgatgcg aacgtgtctg aggcggaagg tgtatacagt 60

gccttggaga agcttggcat cgactgggaa gaggttggaa agcagcttga gctggaaggc 120

gtggactcct tcaagaagag ctttgacagc ctactcgtga gcctgcagga gaagggcaac 180

agcctcaaga tggcgagtgt gtaaagctga gaagattggg tacctgcgag tgaacgattt 240

tactaaataa aatgctagct tgctggctct cctcttagtt tttacgctgt a 291

<210> 507
<211> 244
<212> DNA
<213> Zea mays

<400> 507

aaggcggaag gtgtatacag cgccttggag aagcttggca ttgactgggc cgaggtcgga 60

aagcagcttg agctggaagg tgtggactcc ttcaagaaga gctttgacag cctactcgtg 120

agcctgcagg agaagggcaa cagcctcaag acggcaactg tgtaaaactg agaagattgg 180

gtaccggcgg gtgaacgatt ttactaaata aaatgctagc ttgctggctc tcctaatttt 240

tacg 244

<210> 508
<211> 298
<212> DNA
<213> Zea mays

<400> 508

tgcgaacgtg tctgaggcgg aaggtgtata cagtgccttg gagaagcttg gcatcgactg 60

ggaagaggtt ggaaagcagc ttgagctgga aggcgtggac tccttcaaga agagctttga 120

cagcctactc gtgagcctgc aggagaaggg caacagcctc aagatggcga gtgtgtcaag 180

ctgagaagat tgggtacctg cgagtgaacg attttactaa ataaaatgct agcttgctag 240

ctctcctctt agtttttacg ctgtaccttt gctctcaatt ttctgagtcg gctttgta 298

<210> 509
<211> 241
<212> DNA
<213> Zea mays

<400> 509

gcagaatgtg ttccttccat ccaggaagtt atcgctaatg gcattagcgt caacgtcacg 60

cttattttct caattgcaag atatgaggct gtgattgatg cttacctcga tgggctagag 120

gcttctggct tgagtgaatt atcccgagtt actagcgttg catccttctt tgtcagccga 180

gtggacaccc ttattgacaa aatgcttgac aagattggaa cacctgaggc ccttgccttg 240

a 241

<210> 510
<211> 139
<212> DNA
<213> Zea mays

<400> 510

caagacgcgt gcagtctttt tgagcctatc tacgatgaga ccgatggggc tgatgggtat 60

gtctccgtgg aggtgtctcc taggttggca aatgacactc aaggaactgt tgaggccgca 120

aagtggttac acaaagtgg 139

<210> 511
<211> 170
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 511

cggcactgtc tcgaggacag ttgatgcgaa tgtgcccgac gcggaaggtg tatacagcgc 60

cttggagaag cttggcattg actgggccga ggtcggaaag cagcttgagc tggaaggtgt 120

ggactccttc acagagagca ttgacangct actcgtgagc ctgcaggaga 170

<210> 512
<211> 169
<212> DNA
<213> Zea mays

<400> 512

ctcgatgggc tagaggcttc tggcttgagt gacttatccc gagttactag cgttgcatcc 60

ttctttgtca gccgagtgga caccettatt gacaaaatgc ttgacaagat tggaacacct 120

gaggcccttg ccttgagagg aaaggctgca gtagcgcagg ccaaactag 169

<210> 513
<211> 259
<212> DNA
<213> Zea mays

<400> 513

gcgccttgga gaagcttggc attgactggg gcgaggtcgg aaagcagctt gagctggaag 60

gtgtggactc cttcaagaag acgcggtgac agcctactcg tgagcctaca ggagaagggc 120

aacagcctca agacggcaac tgtgtaaaac tgagaagatt gggtaccggc gggtgaacaa 180

cattactaaa taaaatgcta gcttgctggc tctcttagtt tttacgatgt acctttgctc 240

tccattttct gaatcggga 259

<210> 514

<211> 216
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 514

ggaaagcagc ttgagctgga aggcgtggac tccttcaaga agagctttga cagcctactc 60

gtgagcctgc aggagaaggg caacagcctc aagatggcga gtgtgtaaag ctgagaagat 120

tgggtacctg cgagtgaacg attttactaa atanaatgct agcttgctgg ctctcctctt 180

agtttttacg ctgtactttg ctctcaattt tctgag 216

<210> 515
<211> 291
<212> DNA
<213> Zea mays

<400> 515

catcgactgg gaagaggttg gaaagcagct tgagctggaa ggcgtggact ccttcaagaa 60

gagctttgac agcctactcg tgagcctgca ggagaagggc aacagcctca agatggcgag 120

tgtgtaaagc tgagaagatt gggtacctgc gagtgaacga ttttactaaa taaaatgcta 180

gcttgctggc tctcctctta gtttttacgc tgtacctttg ctctcaattt tctgagtcgg 240

ctttgtatcc cagcttgcca gaacgtcatg tgtagccatg ttcatggctg t 291

<210> 516
<211> 260
<212> DNA
<213> Zea mays

<400> 516

gcgtggactc cttcaagaag agctttgaca gcctactcgt gagcctgcag gagaagggca 60

acagcctcaa gatggcgagt gtgtaaagct gagaagattg ggtacctgcg agtgaacgat 120

tttactaaat aaaatgctag cttgctggct ctcctcttag tttttacgct gtacctttgc 180

tctcaatttt ctgaatcggc tttgtatccc aggcttgcca gaacgtcatt gtgtagccac 240

tgttcatggc ttgtaattgc 260

<210> 517
<211> 327

<212> DNA
<213> Zea mays

<400> 517

cgacggaaat agatgctcgg ttagcttatg acacccaggg cataatccac agggtacatg 60

aactgttgaa tctatacaac caacatgatg tctcaactga ccgcctgtta ttcaaaattc 120

ctgctacatg gcaaggcata gaggcctcaa ggttgcttga atctgaagga attcaaacgc 180

atctatcatt tgtttacagt ttcgcacaag cggcagcggc agcacaagct ggtgcatctg 240

tagtacaaat gtttgtgggc cgattgcggg actgggcagg catcactctg gtgacccaga 300

gatagatgaa gctttgaaga atggaga 327

<210> 518
<211> 203
<212> DNA
<213> Zea mays

<400> 518

cagggcataa tccacagggt acatgaactg ttgaatctat acaaccaaca tgatgtctca 60

actgaccgcc tgttattcaa aattcctgct acatggcaag gcatagaggc ctcaaggttg 120

cttgaatctg aaggaattca aacgcatcta acatttgttt acagtttcgc acaagcggca 180

gggtcagcac aagctggtgc atc 203

<210> 519
<211> 268
<212> DNA
<213> Zea mays

<400> 519

cctcaaggtt gcttgaatct gaaggaattc aaacgcatct aacatttgtt tacagtttcg 60

cacaagcgag cacggcagca caagctggtg catctgtagt acaaatgttt gtaggccgat 120

tgcgggactg ggcaaggcat cactctggtg acccagagat agatgaagct ttgaagaatg 180

gagaagatgc tgggctttct ttggcgaaga aagtatatgc ctatattcac aggaatgggt 240

acaaaacaaa gctgatggcc gctgccat 268

<210> 520
<211> 417

<212> DNA
<213> Zea mays

<400> 520

ggaacacctg aggcccttgc cttgagagga aaggctgcag tagcgcaggc cagactggca 60

aatcggctct ggcagaagaa attctctggc ccaaggtggg aggcgttggc caagaaaggt 120

gccaagaaac aaaggttgtt gtgggcatcc accggtgtca agaacccagc ttatcctgac 180

actctttatg tggacagtct catcggacct gacacggtca acacgatgcc cgaccaagct 240

ttgcaagcat tcatagacca cggcaccgtt tcaaggacag ttgatgcgaa tgtgtctgaa 300

gcggaaggtg tatacagcgc cttggagaag cttggcatcg actgggaaga ggttggaaag 360

cagcttgagc tggaaggcgt ggactccttc aagaagagct ttgacagcct actcgtg 417

<210> 521
<211> 424
<212> DNA
<213> Zea mays

<400> 521

aatcggctct accagaagaa attctctggc ccgaggtggg aggcgttggc caagaaaggt 60

gccatgaaac agaggttgtt gtgggcgttc accggtgtca agaacccagc ttatcccgac 120

actctttaca tcgactgtct cattggacct gacactgtca acacgatgcc cgaccaagct 180

ttgcaggcat tcatagacca cggcactgtt tcgaggacag ttgatgcgaa tgtgtacgag 240

gcggaaggtg tatacagcgc cttggacaat cttggcattg actggcgcga ggtcagaaag 300

cagcttgagc tggaaggtgt ggactccttc atgaagagct ttgacagcct actcgtgagc 360

ctgcaggaga tggtcaacat cctcaagacg gcatctgtgt aaaactgaga agattgtgta 420

ccgg 424

<210> 522
<211> 443
<212> DNA
<213> Zea mays

<400> 522

atttcggctg gaaaggacgc ggagagcgct tactgggaac tcgttataaa ggatatccag 60

gatgcgtgca aactttttga gcccatctac gatgagactg atggggctga tgggtatgtc 120

tccgtagagg tgtctcctag gttggcaaat gacactcaag gaactgttga agcggcaaag 180

tggttacaca aagtggtcaa ccgccccaat gtctacataa agatcccagc tactgcagaa 240

tgtgttcctt ccatccagga agttatcgct aatggcatta gcgtcaacgt cacgcttatt 300

ttctcaattg caagatatga ggctgtgatt gatgcttacc tcgatgggct agaggcttct 360

ggcttgagtg acttatcccg agttactagc gttgcatcct tctttgtcag ccgagtggac 420

acccttattg acaaaatgct tga 443

<210> 523
<211> 438
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 523

gccagcggcg tccgtggagt caccttctac ccaacgattt tccaaaaggc catttgagtc 60

gtccagcgca tatgatgagc agttcaagca gctcatttcg gcaggaaagg atgcggagag 120

cgcttactgg gaactcgtta taaaggatat ccaagatgcg tgcaaacttt ttgagcccat 180

ctacgacgag actgatgggg ctgatgggta tgtctccgta gaggtgtctc ctaggttggc 240

aaatgacact caaggaactg ttgaagcggc aaagtggtta cacaaagtgg tcaaccgccc 300

caatgtctac ataaagatcc cagctactgc agaatgtgtt ccttccatcc aggaagttat 360

cgctaatggc attagcgtca acgtcacgct tatnntctca attgcgagat atgaggctgt 420

gattgatgct tacctcga 438

<210> 524
<211> 369
<212> DNA
<213> Zea mays

<400> 524

gcgagatacg aggctgtgat tgatgcttac cttgatgggc tagaggctgg tggcttgagc 60

gacttatctt gagttaccag cgtcgcatgc ttctttgtca gtcgagtcta cacccttatc 120

gacaaaatgc ttgagaagat tggaacacct gaggcacttg ccttgagagg gaaggctgcc 180

gacgtacagg ccaaactagc aaatcggctc taccagaaga aattctctgg cccgaggtgg 240

gaagcgtctg ccaagaaagg tgccaagaaa cagatgttgt tgcgggcgtt cacccgtgtc 300

aagaacccag cttatcccga cactctttac atcgacagtc ttattggacc tgacacggtc 360

aacacgatt 369

<210> 525
<211> 375
<212> DNA
<213> Zea mays

<400> 525

tgcttacctc gatgggctag aggcttctgg cttgagtgac ttatcccgag ttactagcgt 60

tgcgtccttc tttgtcagcc gagtggacac ccttattgac aaaatgcttg acaagattgg 120

aacacctgag gcccttgcct tgagaggaaa ggctgcagta gcacaggcca aactagcaaa 180

tcggctctac cagaagaaat tctctggccc aaggtgggag gcgttggcca agaaaggtgc 240

caagaaacaa aggttgttgt gggcatccac cggtgtcaag aacccagctt atcctgacac 300

tctggatgtg gacagtctca tctgacctga cacgttcaac acgatgcccg accaagcttt 360

gcaagcattt catag 375

<210> 526
<211> 389
<212> DNA
<213> Zea mays

<400> 526

cccacgcgtc cgctgcgctt catgatctct acgagctcca gggcctgtcc ccgtggtacg 60

agaacctatg ccgccctgtc acagacttgc tgcccattat cgccagcggc gtccgtggag 120

tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc gtccagcgca tatgatgatc 180

agttcaagca gctcatttcg gcaggaaagg atgcggagag cgcttactgg gaactcgtta 240

taaaggatat ccaagatgcg tgcaaacttt ttgagcccat ctacgacgag actgatgggg 300

ctgatgggta tgtctccgta gaggtgtctc ctaggttggc aaatgacact caaggaactg 360

ttgaagcggc aaagtggtta cacaaagtg 389

<210> 527
<211> 379
<212> DNA

<213> Zea mays

<223> unsure at all n locations
<400> 527

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gccatgaaac agaggttgtt gtgggcgtcc accggtgtca agaacccagc ttatcccgac 120

actctctaca tcgacagcct cattggacct gacacggtca acactatgcc cgtacaagct 180

ttgcatgcat tcatagacca cggcactgtt tcgaggacag ttgatgctaa tgtgtacgag 240

gcggaaggtg tatacagcgc cttggagaag cttggcattg actgnggcga ggtcggaaag 300

caacttgagc tggaaggtgt ggactccttc aagaagagct ttgacagcct actcgtgagc 360

ctgcatgaga agggcaaca 379

<210> 528
<211> 185
<212> DNA
<213> Zea mays

<400> 528

aggcctgtcc ccgtggtacg acaacctatg ccgccctgtc acagacttgc tgcccattat 60

cgccagcggc gtccgtggag tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc 120

gtccagcgca tatgatgatc agttcaagca gctcatttcg gcaggaaagg atgcggagag 180

cgcta 185

<210> 529
<211> 374
<212> DNA
<213> Zea mays

<400> 529

gaggtacgcg tacgcgaaca cgatgcccga ccaagctttt caagcattca tagaccactg 60

caccgtttca aggacagttg atgcgaatgt gtctgaggcg gaaggtgtat acagcgcctt 120

ggagaagctt ggcatcgact gggaacaggt tggaaagcag cttgagctgg aacgcgtgga 180

ctccttcaag aagagctttg acagcctact cgtgagcctg caggacaagg gcaacagtct 240

caagatggcg agtgtgtaaa gctgataaga ttgggtacct gccagtgaac gattttacta 300

aataaaatgc tagcttgctg gctcttctct tactatttac gctgtacctt tgctctcaat 360

tatctgaatc ggct 374

<210> 530
<211> 348
<212> DNA
<213> Zea mays

<400> 530

gtctcaactg accgcctgtt attcataatt cctgctacat ggcaaggcat agaggcctca 60

aggttgcttg aatctgaagg aattcaaacg catctaacat ttgtttacag tttcgcacta 120

aagcggcagc ggcagcacaa gctggtgcat ctgtagtaca aatgtttgtg ggccgattgc 180

gggactgggc aaggcatcac tctggtgacc cagagataga tgaagctttg aagaatggag 240

aagatgctgg gctttctttg gcgaagaaag tatatgccta tattcacagg aatgggtaca 300

aaacaaagct gatggccgct gccataccga acaagcagga cgtattta 348

<210> 531
<211> 525
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 531

ggggggtggg gttgactgtc atgttcgcgt ggcggtacaa agtcgaaatt gnccgggcca 60

cccacgcaac cgcatcgcga ccgccaaagc ccgcgacttt cagcctacgg aggccacatc 120

tggccgcgcg ggccgccgct ggcaacgcac ccacgtcccc ggtccgcgag gtcgtcactg 180

agctcgacgc ggtcgccggc ttcagcgaga tcgtgccgga caccgtcgtg ttcgatgatt 240

tcgagaggtt cgcacccacg gcggccacag tgagctcgtc gctgctgctt gggatcactg 300

ggctcccaga cactaagttc aagagtgcga tagatactgc actggcagat ggtgagtgca 360

acgcactgga gaaggctgat gacatgatgt cctgttacct caccaaggct cttgcatatg 420

ttggcgctga actggctcat caagtccctg ggagagtttc gacggaaata gatgctcggt 480

tagcttatga cacccagggc ataatccaca gggtacatga actgt 525

<210> 532
<211> 423
<212> DNA

<213> Zea mays

<223> unsure at all n locations
<400> 532

agagcctcca aaacctcgca acaaccccgt gacacccaca cccatccgcc ctgcgcctcc 60

tcgcgctccc caccaacccc gacgagcggc gatgaccggc acggtgtcca agctggcggc 120

gccccggcct gcggcgccac cgctccggcc ggcgtccctc cgcgccgccg caatcgcctt 180

cgccccctcc ccgcgccggg tccgcgtctc cgtcgccggg cgggccagga tcccctccgt 240

cattgcgatg gcttctgcca aggaaggaaa tggtgcaccg accaagaaaa cctcgcttca 300

cgatctctac gagctccagg gcctctcccc gtggtatgac aacctctgcc gacctgtcac 360

cgacttgctg cccctttatcg ccagcggtgt tcgtggagtc accagcaacc ctgcaattnt 420

cca 423

<210> 533
<211> 429
<212> DNA
<213> Zea mays

<400> 533

cggacgcgtg ggagcctcca aaacctcgca acaaccccgt gacacccaca cccatccgcg 60

ctgcccctcc tcgcgctccc caccaacccc gacgagcggc gatgaccggc acggtgtcca 120

agctggcggc gccccggcct gcggcgccac cgctccggcc ggcgtccctc cgcgccgccg 180

caatcgcctt cgccccctcc ccgcgccggg tccgcgtctc cgtcgccggg cgggccagga 240

tcccctccgt cattgcgatg gcttctgcca aggaaggaaa tggtgcaccg accaagaaaa 300

cctcgcttca cgatctctac gagctccagg gcctctcccc gtggtatgac aacctctgcc 360

gacctgtcac cgacttgctt gcccttatcg gcagcggtgt tcgtggagtc accagcaacc 420

ctacaattt 429

<210> 534
<211> 283
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 534

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ctgattctga gtgttatgga cttgaaaatc ctaacgcgcg attgtcttgt tttgtcaaca 120

aggctttcgc gaatatcggt agtgacatgg caaagcttgt ccctggccgt gtttcgacag 180

aagtggatgc gcggcttgct tatgacacac atgccattat caggaaggtg catgacctgt 240

tgaagttgta catgatannt atgtacctcc gcaacgtctg ttg 283

<210> 535
<211> 250
<212> DNA
<213> Glycine max

<400> 535

agtggacact ctcattgaca aggcccttga gaaaattggc accccagatg ctcttaatct 60

acgtgggaag gtaactgttt attgttttcc aaactaattt ctattcttgg ctttggattt 120

attacacttt caaatgtcaa atatgctctt cggattgcat attgaatttt acaggcagca 180

gtagcccaag cagcattggc ttaccagctc taccaaagga aattttctgg tcaaagtggg 240

aactctaagt 250

<210> 536
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 536

tgtttgatag aaataatgga tcggaacggg ccaaagatca naagtacaat tcttcaccat 60

ctctatgata agcagagaca gagcccttac tatgacaatc tctgtcgccc tgtttcagat 120

ttgcttccat ttattgccaa tgggatcaga ggtgtcacta ccaacccagc ggtactcact 180

actcagtttt ttcttcacct gaaaacatta ctcttctcca tttggtttta tttttatcta 240

gtttctgtgt gttggttata ataacttttc agtgttctca catcgcagat tttgaaaga 300

gctatttcat cctcaaatgc ctacgatgat cag 333

<210> 537
<211> 280
<212> DNA
<213> Glycine max

<400> 537

ggacaccctc attgacaagg cccttgagaa aattggcacc ccagtggccc ttaatctacg 60

cgggaaggca gcggtagccc aagcagcatt ggcttaccag ctctaccaaa ggaaattttc 120

tggtccaagg tgggaagctc tagttaaaaa gggggccaag aagcaaaggc tcctctgggc 180

ctcaaccagt gtaaagaatc ctgcctattc tgacacctta tatgttgctc ctcttattgg 240

acccgacact gtatcaacaa tgccagacca agcccttcaa 280

<210> 538
<211> 294
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 538

gtgttgcctc tttctttgtc agtagagtgg acactctcca ttgacaaggc ccttgagaaa 60

attggcaccc cagaggctct taatctacgt gggaaggcag cagtagccca agcagcattg 120

gcttaccacc tctaccaaag gaaattttct ggtccaaggt gggaagctct agttaaaaag 180

ggggccaaga agcaaaggct ctttgggcct caaccagtgt aaagaaccct gcctattctg 240

acacntatat gttgctcctc tattggaccc gacatgatca accagccaga ccaa 294

<210> 539
<211> 221
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 539

gtagagtgga caccctcatt gacaaggccc ttgagnaaat tggcacccca gtggccctta 60

atctacgcgg gaaggcagcg gtagcccaag cagcattggc ttaccagctc taccaaagga 120

aattttctgg tccaaggtgg gaagctctag ttaaaaaggg ggccaagaag caaaggctcc 180

tctgggcctc aaccagtgta aagaatcctg cctattctga c 221

<210> 540
<211> 299
<212> DNA
<213> Glycine max

<400> 540

tattctcagt ttgcggtgtt tgatagaaat aatggatcgg aacgggccaa agatcaaaag 60

tacaattctt caccatctct atgagaagca gagacagagc ccttactatg acaatctctg 120

tcgccctgtt tcaggtttgc ttccatttat tgccaatggg atcagaggtg tcactaccaa 180

cccagcgatt tttgaaagag ctatttcatc ctcaaatgcc tacgatgatc agttgaggga 240

attggtaggg gcagggaagg acatagaaag tgcttattgg gaattggttg tgaaggaca 299

<210> 541
<211> 240
<212> DNA
<213> Glycine max

<400> 541

gaagcagaga cagagccctt actatgacaa tctctgtcgc cctgtttcag atttgcttcc 60

atttattgcc aatgggatca gaggtgtcac taccaaccca gcgatttttg aaagagctat 120

ttcatcctca aaatgctacg atgatcagtt gagggaaatg gtcagggcca ggaaggacat 180

agaaagtgct tattgggaat tggttgtgaa ggacatacag gatacttgca aacttctgga 240

<210> 542
<211> 278
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 542

tttcacttgc tctctctttg ctcttatccc ttttcctttn tctncttttc ctttgggttt 60

tctattctca gtttgcggtg tttgatagaa ataatggatc ggaaccggcc aaagatcaaa 120

agtacaattc ttcaccatct ctatgagaag cagagacaga gcccttacta tgacaatctc 180

tgtcgccctg tttcagattt gcttccattt attgccaatg ggatcagagg tgtcactacc 240

aacccagcga tttttganag agctatttca tcctcaag 278

<210> 543
<211> 254
<212> DNA
<213> Glycine max

<400> 543

atttttcttt tttcttcttt tcctttgggt tttctattct cagtttgcgg tgtttgatag 60

aaataatgga tcggaacggg ccaaagatca aaagtacaat tcttcaccat ctctatgaga 120

agcagagaca gagcccttac atgacaatct ctgtcgccct gtttcagatt tgcttccatt 180

tattgccaat gggatcagag gtgtcactac caacccagcg atttttgaaa gagctatttc 240

atcctcaaat gcct 254

<210> 544
<211> 236
<212> DNA
<213> Glycine max

<400> 544

caagaagcaa aggctccttt gggcctcaac cagtgtaaag aaccctgcct attctgacac 60

cttatatgtt gctcctctta ttggacccga cactgtatca accatgccag accaagccct 120

tcaagcattt attgatcatg gtaccgtatc caggacaata gactcaaatg catctgaagc 180

tgaaggaata tacaatgctc tccagaaatt gggtattgac tggagctttg ttggtt 236

<210> 545
<211> 260
<212> DNA
<213> Glycine max

<400> 545

ggctcctttg ggcctcaacc agtgtaaaga accctgccta ttctgacacc ttatatgttg 60

ctcctcttat tggacccgac actgtatcaa ccatgccaga ccaagccctt caagcattta 120

ttgatcatgg taccgtatcc aggacaatag actcaatgca tctgaagctg aaggaatata 180

caatgctctc cagaaattgg gtattgactg gagctttgtt ggttcccagc ttgaacttga 240

aggagtggac tcgtttaaga 260

<210> 546
<211> 250
<212> DNA
<213> Glycine max

<400> 546

gaaggaatat acaatgctct ccagaaattg ggtattgact ggagctttgt tggttcccag 60

cttgaacttg aaggagtgga ctcgtttaag aagagctttg acagcctcct ggattctctg 120

caagagaagg caaactctct taagttggtc agccattgaa gtgtgaacgt catagttagt 180

aatgcagtgc tatgtatgaa gtgatttatg gattaataaa aggcagtggc tgtgcatttt 240

gtgctgctgt 250

<210> 547
<211> 265
<212> DNA
<213> Glycine max

<400> 547

ctcgagccgg gaatatacaa tgctctccag aaattgggta ttgactggag ctttgttgga 60

ctcccagctt gaacttgaag gagtggactc gtttaagaag agctttgaca gcctcctgga 120

ttctctgcaa gagaaggcaa actctcttaa gttggtcagc cactgaagtt tgaacgtcat 180

ggttagtaat gcagtgctgt gtatgatggc atctatggat taataaaagg cagcggctgt 240

gcattttgtg ctgctgcaaa tgtgc 265

<210> 548
<211> 228
<212> DNA
<213> Glycine max

<400> 548

cgtcatggtt gctcctctta ttggacccga cactgtatca accatgccag accaagccct 60

tcaagcattt attgatcatg gtaccgtatc caggacaata gactcaaatg tgcttcatgg 120

agtcatttat ttagacgata gtgatacaat gtaaatggga aaaattgtcc gcttcaagtc 180

aagcgttttg ttttttcccc actatacaat ggttgtgcgt ttatgttt 228

<210> 549
<211> 224
<212> DNA
<213> Glycine max

<400> 549

cgtcatggat gctcctctta ttggacccga cactgtatca accatgccag accaagccct 60

tcaagcattt attgatcatg gtaccgtatc caggacaata gactcaaatg tgcttcatgg 120

agtcatttat ttagacgata gtgatacaat gtacttggga aaaattgtcc gcttcaagtc 180

aagcgttttg ttttttcccc actatacaat ggttgtgcga ttat 224

<210> 550
<211> 238
<212> DNA
<213> Glycine max

<400> 550

gatcaaatgc tcccaaacag atgggaatgg aagtcctgca aagaggacag tgcttcatga 60

tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga 120

ccttcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgatttttca 180

gaaagctatc tcatcatcga atgcttacaa tgatcagttc agggaacttg tgcaagca 238

<210> 551
<211> 269
<212> DNA
<213> Glycine max

<400> 551

ggaatggaag tcctgcaaag aggacagtgc ttcatgatct ttatgagaaa gaagggcaga 60

gtccatggta tgataatctc tgcagacctg ttacagacct gcttcctctt atagcaagtg 120

gtgtcagagg cgtcactagc aaccctgcga tctttcagaa agctatctca tcatcgaatg 180

cttacaatga tcagttcagg gaacttgtgc aaacagggaa agacattgaa agtgcatatt 240

gggaacttgt agtgaaggat atccaagat 269

<210> 552
<211> 272
<212> DNA
<213> Glycine max

<400> 552

aattaacctc tccgcttccc tccgatccat tcactccctc cctcttaaaa cctccttgcg 60

gatcaaatgc tcccaaacag atgggaatgg aagtcctgca aagaggacag tgcttcatga 120

tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga 180

cctcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgatttttca 240

gaaagctatc tcatcatcga atgcttacaa tg 272

<210> 553
<211> 231
<212> DNA
<213> Glycine max

<400> 553

gctccctctt aaaacctcct tacggatcaa atgctcccaa acagatggga atggaagtcc 60

tgcaaagagg acagtgcttc atgatcttta tgagaaagaa gggcagagtc catggtatga 120

taatctctgc agacctgtta cagacctgct tcctcttata gcaagtggtg tcagaggcgt 180

cactagcaac cctgcgatct ttcagaaagc tatctcatca tcgaatgctt a 231

<210> 554
<211> 237
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 554

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ttncggatca aatgctccca aacagatggg aatggaagtc ctgcaaagag gacagtgctt 120

catgatcttt atgagaaaga acngcagagt ccatggtatg ataatctctg cagacctgtt 180

acagaccttc ttcctcttat agcaagtggt gtcagaggng tcactagcaa ccctgng 237

<210> 555
<211> 270
<212> DNA
<213> Glycine max

<400> 555

taaaactaac ctatccgctt ccctccgatc cattcactcg ctccctctta aaacctcctt 60

acggatcaaa tgctcccaaa cagatgggaa tggaagtctg caaagaggac agtgcttcat 120

gatctttatg agaaagaagg gagagtccat ggtatgataa tctctgcaga cctgttacag 180

actgcttctc ttatagcaag tggtgtcaga ggcgtcatta gcaacctgcg catctttcag 240

aaagctatct catcatcgaa tgttacatga 270

<210> 556
<211> 292
<212> DNA
<213> Glycine max

<400> 556

ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca 60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaagaagg gcagagtcca tggtatgata atctctgcag acctgttaca ga 292

<210> 557
<211> 165
<212> DNA
<213> Glycine max

<400> 557

caaaattaac ctctccgctt ccctccgatc cattcactcc ctccctctta aaacctcctt 60

gcggatcaaa tgctcccaaa cagatgggaa tggaagtcct gcaaagagga cagtgcttca 120

tgatctttat gagaaagaag ggcagagtcc atggtatgat aatct 165

<210> 558
<211> 289
<212> DNA
<213> Glycine max

<400> 558

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agattctcgc ttcctctcct tcaatccttc ttccaacgct attaattaca aaattaacct 120

ctccgcttcc ctccgatcca ttcactccct ccctcttaaa acctccttgc ggatcacctg 180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga 240

gaaagaaggg cagagtccat ggtatgataa tctctgcaga cctgttaca 289

<210> 559
<211> 275

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 559

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

aganagaagg gcagagtcca tggtatgata atctc 275

<210> 560
<211> 274
<212> DNA
<213> Glycine max

<400> 560

attttcaagc tctcaacgcc atctccagct gcttccttat cagaagcgct tcgccccaga 60

gattctcgct tcctctcctt caatccttct tccaacgcta ttaattacaa aattaacctc 120

tccgcttccc tccgatccat tcactcctcc ctcttaaaac ctccttgcgg atcaaatgct 180

cccaaacaga tgggaatgga agtcctgcaa agaggacagt gcttcatgat ctttatgaga 240

aagaagggca gagtccatgg tatgataatc tctg 274

<210> 561
<211> 270
<212> DNA
<213> Glycine max

<400> 561

ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca 60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatca ttcactccct ccctcttaaa acctccttgc ggatcaaatg 180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga 240

gaaagaaggg cagagtccat ggtatgataa 270

<210> 562

<211> 265
<212> DNA
<213> Glycine max

<400> 562

cgcctccatt ttcaagctct caacgccatc tccagctgct tccttatcag aagcgcttcg 60

ccccagagat tctcgcttcc tctccttcaa tccttcttcc aacgctatta attacaaaat 120

taacctctcc gcttccctcc gatccattca ctccctccct cttaaaacct ccttgcggat 180

caaatgctcc caaacagatg ggaatggaag tcctgcaaag aggacagtgc ttcatgatct 240

ttatgagaaa gaagggcaga gtcca 265

<210> 563
<211> 261
<212> DNA
<213> Glycine max

<400> 563

attttcaagc tctcaacgcc atctccagct gcttccttat cagaagcgct tcgccccaga 60

gattctcgct tcctctcctt caatccttct tccaacgcta ttaattacaa aattaacctc 120

tccgcttccc tccgatccat tcactccctc cctcttaaaa cctccttgcg gatcaaatgc 180

tcccaaacag atgggaatgg aagtcctgca aagaggacag tgcttcatga tctttatgag 240

aaagaagggc agagtccatg g 261

<210> 564
<211> 282
<212> DNA
<213> Glycine max

<400> 564

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agagattctc gcttcctctc cttcaatcct tcttccaacg ctattaatta cacaattaac 120

ctctccgctt ccctccgatc cattcactcc ctccctctta aaacctcctt gcggatcaaa 180

tgctcccaaa cagatgggaa tggaagtcct gcaaagagga cagtgcttca tgatctttat 240

gagaaagaag ggcagagtcc atggtatgat aatctctgca ga 282

<210> 565

<211> 290
<212> DNA
<213> Glycine max

<400> 565

tccgcttcgt gacttgcagc aattcccaat ggcttccgtt tccaagctct caacgccaaa 60

tccacttgct tccttatcag aagcgcttcg cccccgagat tctcgcttcc tcaccttcaa 120

accttcttcc atcgctttta atcacaaaac taacctatcc gcttccctcc gatccattca 180

ctcgctccct cttaaaacct ccttacggat caaatgctcc caaacagatg ggaatggaag 240

tcctgcaaag aggacagtgc ttcatgatct ttatgagaaa gaagggcaga 290

<210> 566
<211> 256
<212> DNA
<213> Glycine max

<400> 566

ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca 60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaagaagg gcagag 256

<210> 567
<211> 271
<212> DNA
<213> Glycine max

<400> 567

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acttgcttcc ttatcagaag cgcttcgccc ccgagattct cgcttcctca ccttcaaacc 120

ttcttccatc gcttttaatc acaaaactaa cctatccgct tccctccgat ccattcactc 180

gctccctctt aaaacctcct tacggatcaa atgctcccaa acagatggga atggaagtcc 240

tgcaaagagg acagtgcttc atgatcttta t 271

<210> 568

<211> 284
<212> DNA
<213> Glycine max

<400> 568

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ctgcttcctt atcagaagcg cttcgcccca gagattctcg cttcctctcc ttcaatcctt 120

cttccaacgc tattaattac aaaattaacc tctccgcttc cctccgatcc attcactccc 180

tccctcttaa aacctccttg cggatcaaat gctcccaaac agatgggaat ggaagtcctg 240

caaagaggac agtgcttcat gatctttatg agaaagaagg gcag 284

<210> 569
<211> 264
<212> DNA
<213> Glycine max

<400> 569

ctgacttgca gcaattccca atggcttccg tttccaagct ctcaacgcca aatccacttg 60

cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaaccttctt 120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc 180

ctcttaaaac ctccttacgg atcaaatgct cccaaacaga tgggaatgga agtcctgcaa 240

agaggacatg cttcatgatc ttta 264

<210> 570
<211> 250
<212> DNA
<213> Glycine max

<400> 570

caatggcctc cattttcaag ctctcaacgc catctccagc tgcttcctta tcagaagcgc 60

ttcgccccag agattctcgc ttcctctcct tcaatccttc ttccaacgct attaattaca 120

aaattaacct ctccgcttcc ctccgatcca ttcactccct ccctcttaaa acctccttgc 180

ggatcaaatg ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg 240

atctttatga 250

<210> 571

<211>	272
<212>	DNA
<213>	Glycine max

<400>	571

ctcgagccga gcaattccca atggcttccg tttccaagct ctcaacgcca aatccacttg 60

cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaacctactc 120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc 180

ctcttaaaac ctccttacgg atcaaatgct cccaaacaga tgggaatgga agtcctgcaa 240

cgaggacagt gcttcatgat ctttatgaga aa 272

<210>	572
<211>	272
<212>	DNA
<213>	Glycine max

<400>	572

cgcttcgtga cttgcagcaa ttcccaatgg cttccgtttc caagctctca acgccaaatc 60

cacttgcttc cttatcagaa gcgcttcgcc cccgagattc tcgcttcctc accttcaaac 120

cttcttccat cgcttttaat cacaaaacta acctatccgc ttccctccga tccattcact 180

cgctccctct taaaacctcc ttacggatca aatgctccca aacagatggg aatggaagtc 240

ctgcaaagag gacagtgctt catgatcttt at 272

<210>	573
<211>	237
<212>	DNA
<213>	Glycine max

<400>	573

ctcaacgcca tctccagctg cttccttatc agaagcgctt cgccccagag attctcgctt 60

cctctccttc aatccttctt ccaacgctat taattacaaa attaacctct ccgcttccct 120

ccgatccatt cactccctcc ctcttaaaac ctccttgcgg atcaaatgct cccaaacaga 180

tgggaatgga agtcctgcaa agaggacagt gcttcatgat ctttatgaga aagaagg 237

<210>	574
<211>	251
<212>	DNA

<213> Glycine max

<400> 574

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ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca    60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagaagg g                                                        251
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<210> 575
<211> 233
<212> DNA
<213> Glycine max

<400> 575

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ctgacttgca gcaattccca atggcttccg tttccaagct ctcaacgcca aatccacttg    60

cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaaccttact   120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc   180

ctcttaaaac ctccttacgg atcaaatgct cccaaacaga tgggaatgga agt          233
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<210> 576
<211> 279
<212> DNA
<213> Glycine max

<400> 576

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagacgg gcagagtcca tggtatgatc atctctgca                          279
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<210> 577
<211> 244
<212> DNA
<213> Glycine max

<400> 577

ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca 60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc ctccgatcca ttcactccct ccctcttaaa acctccttgc ggatcaaatg 180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga 240

gaaa 244

<210> 578
<211> 249
<212> DNA
<213> Glycine max

<400> 578

caagctctca acgccatctc cagctgcttc cttatcagaa gcgcttcgcc ccagagattc 60

tcgcttcctc tccttcaatc cttcttccaa cgctattaat tacaaaatta acctctccgc 120

ttccctccga tccattcact ccctccctct taaaacctcc ttgcggatca aatgctccca 180

aacagatggg aatggaagtc ctgcaaagag gacagtgctt catgatcttt atgagaaaga 240

gggcagagt 249

<210> 579
<211> 245
<212> DNA
<213> Glycine max

<400> 579

ccattttcaa gctctcaacg ccatctccag ctgcttcctt atcagaagcg cttcgcccca 60

gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaa 245

<210> 580
<211> 293
<212> DNA
<213> Glycine max

<400> 580

gctatctcat catcgaatgc ttacaatgat cagttcaggg aacttgtgca aacagggaaa 60

gacattgaaa gtgcatattg ggaacttgta gtgaaggata tccaagatgc ttgcagacta 120

tttgaaccaa tctatgatca aacagatggt ggtgatggta tgtttctgtt gaagtatctc 180

ctaggctcgc tgatgacact gagggaacca tagaagctgc aaaatggctt cataaagtgg 240

ttgatcgccc caatgtgtat attaagattc ctgctacaga ggcatgtgtg cct 293

<210> 581
<211> 271
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 581

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tcagaaagct atctcatcat cgaatgctta caatgatcag ttcagggaac ttgtgcaaac 120

agggaaagac attgaaagtg catattggga acttgtagtg aaggatatcc aagatgcttg 180

cagactattt gaaccaatct atgatcaaac agatggtggt gatgggtatg tttctgtnga 240

agtatctcct aggctcgctg atgacactga g 271

<210> 582
<211> 274
<212> DNA
<213> Glycine max

<400> 582

ctagatgctt gcaaattatt tgaaccaatc tatgatcaaa cagatggtgg tgatggctat 60

gtttctgttg aagtatctcc caggctcgct gatgacactg agggaaccat agaagctgca 120

aaatggcttc ataaagtggt tgatcgcccc aatgtgtata ttaagattcc tgctacagag 180

gcatgtgtgc cttcaattaa ggaagttatt gctaatggga taagtgtgaa tgtgacgctg 240

atattctctc ttgcaagata tgaagctgta atag 274

<210> 583
<211> 267
<212> DNA
<213> Glycine max

<400> 583

aagacattga aagtgcatat tgggaacttg tagtgaagga tatccaagat gcttgcaaat 60

tatttgaacc aatctatgat caaacagatg gtggtgatgg ctatgtttct gttgaagtat 120

ctcccaggct cgctgatgac actgagggaa ccatagaagc tgcaaaatgg cttcataaag 180

tggttgatcg ccccaatgtg tatattaaga ttcctgctac agaggcatgt gtgccttcaa 240

ttaaggacgt tattgctaat gggataa 267

<210> 584
<211> 248
<212> DNA
<213> Glycine max

<400> 584

agaaagtgca tattgggaac ttgtagtgaa ggatatccaa gatgcttgca gactatttga 60

accaatctat gatcaaacag atggtggtga tgggtatgtt tctgttgaag tatctcctag 120

gctcgctgat gacactgagg gaaccataga agctgcaaaa tggcttcata aagtggttga 180

tcgccccaat gtgtatatta agattcctgc tacagaggca tgtgtgcctt caattaagga 240

agttattg 248

<210> 585
<211> 253
<212> DNA
<213> Glycine max

<400> 585

gcgattactc agaaagctat ctcatcatcg actccttaca atgatcagtt cagggaactt 60

ctgcaagcag ggaaagacat tgaaagtgca tattgggaac ttgtagtgaa ggatatccaa 120

gatgcttgca aattatttga accaatctat gatcaaacag atggtggtga tggctatgtt 180

tctgttgaag tatctcccag gctcgctgat gaacctgagg gaaccatagc agctgcaaaa 240

tggcttcata aag 253

<210> 586
<211> 253
<212> DNA
<213> Glycine max

<400> 586

gaagctgcaa aatggcttca taaagtggtt gatcgcccca atgtgtatat taagattcct 60

gctacagagg catgtgtgcc ttcaattaag gaagttattg ctaatgggat aagtgtgaat 120

gtgacgctga tattctctct tgcaagatat gaagctgtaa ttgatgcata cttggatggt 180

cttgaggcat ctgagttaaa tgacctctct agagttacaa gtgttgcctc tttcttcgtc 240

agtagagtgg aca 253

<210> 587
<211> 264
<212> DNA
<213> Glycine max

<400> 587

ctcgagccta agacattgaa agtgcatatt gggaacttgt agtgaaggat atccaagatg 60

cctgcagact atttgaacca atctatgatc aaacagatgg tggtgatggg tatgtttctg 120

ttgaagtatc tcctaggctc gctgatgaca ctgagggaac cattgaagct gcaaaatggc 180

ttcataaagg gttgatcgcc ccaatgtgta tattaagatt cctgctacag aggcatgtgt 240

gccttcaatt aaggaagtta ttgc 264

<210> 588
<211> 263
<212> DNA
<213> Glycine max

<400> 588

ctgatattct ctcttgcaag atatgaagct gtaatagatg cttacttgga tggtcttgag 60

gcatctgggt taaatgacct ctctagagtt acaagtgttg cctctttctt tgtcagtaga 120

gtggacactc tcattgaaag gcccttgaga aaattggcac cccagaggct cttaatctac 180

gtgggaaggc agcagtagcc caagcagcat tggcttacca gctctaccaa aggaaatttt 240

ctggtccaag gtgggaagct cta 263

<210> 589
<211> 244
<212> DNA
<213> Glycine max

<400> 589

gggataagtg tgaatgtgac gctgatattc tctcttgcaa gatatgaagc tgtaatagat 60

gcttacttgg atggtcttga ggcatctggg ttaaatgacc tctctagagt tacaagtgtt 120

gcctctttct ttgtcagtag agtggacact ctcattgaca aggcccttga gaaaattggc 180

accccagagg ctcttaatct acgtgggaag gcagcagtag cccaagcagc attggcttac 240

cagc 244

<210> 590
<211> 228
<212> DNA
<213> Glycine max

<400> 590

gcttacaatg atcagttcag ggaacttgtg caaacaggga aagacattga aagtgcatat 60

tgggaacttg tagtgaagga tatccaagat gcttgcagac tatttgaacc aatctatgat 120

caaacagatg gtggtgatgg gtatgtttct gttgaagtat ctcctaggct cgctgatgac 180

actgagggaa ccatagaagc tgcaaaatgg cttcataaag tggttgat 228

<210> 591
<211> 265
<212> DNA
<213> Glycine max

<400> 591

catagaagct gcaaaatggc ttcataaagt ggttgatcgc cccaatgtgt atattaagat 60

tcctgctaca gaggcatgtg tgccttcaat taaggaagtt attgctaatg ggataagtgt 120

gaatgtgacg ctgatattct ctcttgcaag atatgaagct gtaatagatg cttacttgga 180

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tgtcagtaga gtggacactc tcatt 265

<210> 592
<211> 281
<212> DNA
<213> Glycine max

<400> 592

cctcgagccg attcggctcg agcgaatgct tacaatgatc agttcaacgg aacttgtgca 60

aacagggaaa gacattgaaa gtacatattg ggaacttgta gtgaaggata tccaagatgc 120

ttgcagacta tttgaaccaa tctatgatca aacagatggt ggtgatgggt atgtttctgt 180

tgaagtatct cctaggctcg ctgatgacac tgagggaacc atagaagctg caaaatggct 240

tcataaagtg gttgatcgcc ccaatgtgta tattaagatt c 281

<210> 593
<211> 281
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 593

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aaagtgcata ttgggaactt gtagtgaagg atatcnaaaa tgcnaaaaan gananttgaa 120

accaatctat gancaaacag atggnggtga tgggtatgtt tctgttgaag tatctcctag 180

ggctcgctga tgaacactga gggaaccata gaagctgcaa aatggcttca taaagtggnt 240

gatcggccca atgtgtatat taagattcct gnttacagag g 281

<210> 594
<211> 260
<212> DNA
<213> Glycine max

<400> 594

gccttcaatt aaggaagtta ttgctaatgg gataagtgtg aatgtgacgc tgatattctc 60

tcttgcaaga tatgacgctg taatagatgc ttacttggat ggtcttgagg catctgggtt 120

aaatgacctc tctagagtta caagtgttgc ctctttcttt gtcagtagag tggacactct 180

cattgacaag gcccttgaga aaattggcac cccagaggct cttaatctac gtgggaaggc 240

agcagtagcc caagcagcat 260

<210> 595
<211> 217
<212> DNA
<213> Glycine max

<400> 595

gaagttattg ctaatgggat aagtgtgaat gtgacgctga tattctctct tgcaagatat 60

gaagctgtaa ttgatgcata cttggatggt cttgaggcat ctgagttaaa tgacctctct 120

agagttacaa gtgttgcctc tttcttcgtc agtagagtgg acaccctcat tgacaaggcc 180

cttgagaaaa ttggcacccc agtggccctt aatctac 217

<210> 596
<211> 212
<212> DNA
<213> Glycine max

<400> 596

ctatgatcaa acagatggtg ctgatggcta tgtttctgtt gaactatctc ccaggctcgc 60

tgatgacact gagggaacca tagaagctgc aaaatggctt cataaagtgg ttgatcgccc 120

caatgtgtat attaagattc ctgctacaga ggcatgtgtg ccttcaatta aggaagttat 180

tgctaatggg ataagtgtga atgtgacgct ga 212

<210> 597
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 597

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cgcatcatcg aaggnttacn atgatcngtt cagggaactt ggtgcaagca gggaaagaca 120

ttgaaagtgc atattgggaa ctngtagtga aggatatcca agatgcttgc aaattatttg 180

aaccantcta tnatcaaaca gatggtggtg atggctatgt ttctgttgaa gtatctccca 240

ggctcgctga tgacactgag gganccatag aactgcaaaa tggcttcat 289

<210> 598
<211> 260
<212> DNA
<213> Glycine max

<400> 598

gtgaatgtga cgctgatatt ctctcttgca agatatgaag ctgtaattga tgcatacttg 60

gatggtcttg aggcatctga gttaaatgac ctctctagag ttacaagtgt tgcctctttc 120

ttcgtcagta gagtggacac cctcattgac aaggcccttg agaaaattgg caccccagtg 180

gcccttaatc tacgcgggaa ggcagcggta gcccaagcag cattggctta ccagctctac 240

caaaggaaat tttctggtcc 260

<210> 599
<211> 229
<212> DNA
<213> Glycine max

<400> 599

taaggaagtt attgctaatg gactaagtgt gaatgtgacg ctgatattct ctcttgcaag 60

atatgaagct gtaattgatg catacttgga tggtcttgag gcatctgagt taaatgacct 120

ctctagagtt acaagtgttg cctctttctt cgtcagtaga gtggacaccc tcattgacaa 180

ggcccttgag gaaattggca ccccagtggc ccttaatcta cgcgggaag 229

<210> 600
<211> 182
<212> DNA
<213> Glycine max

<400> 600

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ctggatggtc ttgaggcatc tgagttaaat gacctctcta gagttacaag tgttgcctct 120

ttcttcgtca gtagagtgga caccctcatt gacaaggccc ttgagaaaat tggcacccca 180

gt 182

<210> 601
<211> 399
<212> DNA
<213> Glycine max

<400> 601

gatgaatcca tctcttccat gaaggaggtc atttctttgg ggataagtgt aaatgccact 60

ctcatattct gcctccctaa atatgaagca gtgattgatg cttacttgga tggccttgag 120

tcttgtggca tgactgatct ctctaaggtt tcaagtgcag cagcattcta catcagtaga 180

gtggatgtta cacttgacaa gaaacttgag caaattggta ctactgaggc tcttgatctc 240

aaaggaaagg gtgcggttgc tcaagcagtc ttagcatacc aactttacca gaaaaaattt 300

tctggtccaa gatgggaacg cttggagaat agaagtgcca agaagcagag gttgatgtgg 360

gcttcaacaa atgtgaaaaa tccatcttac cctgacaca 399

<210> 602
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 602

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tcagtagaat ggacaccctc attgacaagg cccttgagaa aattggcacc ccaatggccc 120

ttaatctacg tgggaaggca acggtagccc aagcagcatt ggcttaacag ctctaccaaa 180

gaaattttct ggtccaaagt gggaagctct agttaaaaag ggggccaaga agcaaaggct 240

cctctgggcc ttaaccagtg taaagaatcc tgcctattct gacaccttat atgttgctcc 300

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tcatggtacc gtatccagga caatagactc anatgcatct gaagc 405

<210> 603
<211> 399
<212> DNA
<213> Glycine max

<400> 603

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cccttactat gacaatctct gtcgccctgt ttcagatttg cttccattta ttgccaatgg 120

gatcagaggt gtcactacca acccagcgat ttttgaaaga gctatttcat cctcaaatgc 180

ctacgatgat cagttgaggg aattggtagg ggcagggaag gacatagaaa gtgcttattg 240

ggaattggtt gtgaaggaca tacaggatac ttgcaaactt ctggagccaa tttacaatga 300

aacagatggg gaagatggac atgtatctct tgcagtttcc ccaaagctag caaatgacac 360

caaggggaca attgaggcag caaaatggct tcataatat 399

<210> 604
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 604

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tcaaatgcat ctgaagctga aggaatatac aatgctctcc agaaattggg tattgactgg 120

agctttgttg gttcccagct tgaacttgaa ggagtggact cgtttaagaa gagctttgac 180

agcctcctgg attctctgca agagaaggca aactctctta agttggtcag ccactgaagt 240

ttgaacgtca tggttagtaa tgcagtgctg tgtatgatgg catctatgga ttaataaaag 300

gcagcggctg tgcattttgt gctgctgcan atgtgcttca tggagtcatt tatttagacg 360

atagtgatac aatgtaaatg ggaaaaattg tccgcttcaa gtcaagcgtt ttgttttt 418

<210> 605
<211> 396
<212> DNA
<213> Glycine max

<400> 605

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caatccttct tccaacgcta ttaattacaa aattaacctc tccgcttccc tccgatccat 120

tcactccctc cctcttaaaa cctccttgcg gatcaaatgc tccaaacaga tgggaatgaa 180

gtcctgcaaa gaggacagtg cttcatgatc tttatgagaa agaagggcag agtccatggt 240

atgataatct ctgcagacct gttacagacc ttcttcctct tatagcaagt ggtgtcagag 300

gcgtcactag caaccctgcg atttttcaga aagctatctc atcatcgaat gcttacaatg 360

atcagttcag ggaacttgtg caagcaggga aagaca 396

<210> 606
<211> 428
<212> DNA
<213> Glycine max

<400> 606

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gaggttctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaagatag gcagagtcca tggtatgata atctctgcag acctgttaca gaccttctta 300

ctcttatagc aagtggtgtc agaggcgtca ctagcaaccc tgcgattttt cagaaagcta 360

tctcatcatc gaatgcttac aatgatcagt tcaaggaact tgtgcaagca tggaaagaca 420

ttgaaagt 428

<210> 607
<211> 373
<212> DNA
<213> Glycine max

<400> 607

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ctgcttcaat ccttatgcca acgctatcaa ttacaaaatt gacctctccg cttgcctccg 120

atccattcac tccctgccta ttaaaaccta cttgcggatc aaatgctccc aaacagatgg 180

gaatggaagt cctgctaaga ggacagcgct tcatgatctt tatgagaaag aagggcagag 240

tccatggtat gataatctct gcagacctgt tacagagctt gttcctgtta tagcacgtgg 300

tgtcagaggc gtcactagca accctgcgat tttcagaaa gctatctcat catcgaatgc 360

ttacaatgat cag 373

<210> 608
<211> 405
<212> DNA
<213> Glycine max

<400> 608

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agaagcgctt cgccccagag attctcgctt cctctccttc aatccttctt ccaacgctat 120

taattacaaa attaacctct ccgcttccct ccgatccatt cactccctcc ctcttaaaac 180

ctccttgcgg atcaaatgct cccaaacaga tgggaatgga agtcctgcaa agaggacagt 240

gcttcatgat ctttatgaga aagaaaggca gagtccatgg tatgataatc tctgcagacc 300

tgttacagac cttcttcctc ttatagcaag tggtgtcaga ggcgtcacta gcaaccctgc 360

gatttttcag aaagctatct catcatcgaa tgcttacaat gatca 405

<210> 609
<211> 417
<212> DNA
<213> Glycine max

<400> 609

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aatggcctcc attttcaagc tctcaacgcc atctccagct gcttccttat cagaagcgct 120

tcgccccaga gattctcgct tcctctcctt caatccttct tccaacgcta ttaattacaa 180

aattaacctc tccgcttccc tccgatccat tcactccctc cctcttaaaa cctccttgcg 240

gatcaaatgc tcccaaacag atgggaatgg aagtcctgca aagaggacag tgcttcatga 300

tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga 360

ccttcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgatttt 417

<210> 610
<211> 414
<212> DNA
<213> Glycine max

<400> 610

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agaagacgac agaaggggac tccatcctcc gcttcgtgac ttgcagcaat tcccaatggc 120

ttccgtttcc aagctctcaa cgccaaatcc acttgcttcc ttatcagaag cgcttcgccc 180

ccgagattct cgcttcctca ccttcaaacc ttcttccatc gcttttaatc acaaaactaa 240

cctatccgct tccctccgat ccattcactc gctccctctt aaaacctcct tacggatcaa 300

atgctcccaa acagatggga atggaagtcc tgcaaagagg acagtgcttc atgatcttta 360

tgagaaagaa gggcagagtc catggtatga taatctctgc agacctgtta caga 414

<210> 611
<211> 454
<212> DNA
<213> Glycine max

<400> 611

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc 120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaagaagg gcagagtcca tggtatgata atctctgcag acctgttaca gaccttcttc 300

ctcttatagc aagtggtgtc agaggcgtca ctagcaaccc tgcgattttt cagaaagcta 360

tctcatcatc gaatgcttac aatgatcagt tcacggaact tgtgcaagcg ggaaagacat 420

ttgaagtgca tattgggaac ttgtaatgaa agat 454

<210> 612
<211> 389
<212> DNA
<213> Glycine max

<400> 612

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cccagagatt ctcgcttcct ctccttcaat ccttcttcga acgctattaa ttacaaaatt 120

aacctctccg cttccctccg atccattcac tccctccctc ttaaaacctc cttgcggatc 180

aaatgctccc aaacagatgg gaatggaagt cctgcaaaga ggacagtgct tcatgatctt 240

tatgagaaag aagggcagag tccatggtat gataatctct gcagacctgt tacagacctt 300

cttcctctta tagcaagtgg tgtcagaggc gtcactagca accctgcgat tttcagaaa 360

gctatctcat catcgaatgc ttacaatga 389

<210> 613
<211> 384
<212> DNA
<213> Glycine max

<400> 613

tcaacgccat ctccagctgc ttccttatca gaagcgcttc gccccagaga ttctcgcttg 60

gtctccttca atccttcttc caacgctatt aattacaaaa ttaacctctc cgcttccctc 120

cgatccattc actccctacc tcttaaaacc tacttgcgga tcaaatgctc ccaaacagat 180

gggaatggaa gtcctgcaaa gaggacagtg cttcatgatc tttatgagaa agataggcag 240

aatccatgga atgacaatct ctgcaaacct gttacagacc ttcttcctct tatagcaagt 300

ggtgtcagag gcgtcactag gcaccctgcg atttttcaga aagctatctc atcatcgaat 360

gcttacaatg atcaattcaa ggaa 384

<210> 614
<211> 408
<212> DNA
<213> Glycine max

<400> 614

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tcccaggctc gctgatgaca ctgagggaac catagaagct gcaaaatggc ttcataaagt 180

ggttgatcgc cccaatgtgt atattaagat tcctgctaca gaggcatgtg tgccttcaat 240

taaggaagtt attgctaatg ggataagtgt gaatgtgacg ctgatattct ctcttgcaag 300

atatgaagct gtaatagatg cttacttgga tggtcttgag gcatctgggt taaatgacct 360

gtctagagtt acaagtgttg cctctttctt tgtcagtaga gtggacac 408

<210> 615
<211> 434
<212> DNA
<213> Glycine max

<400> 615

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tatgtttctg ttgaagtatc tcccaggctc gctgatgaca ctgagggaac catagaagct 120

gcaaaatggc ttcataaagt ggttgatcgc cccaatgtgt atattaagat tcctgctaca 180

gaggcatgtg tgccttcaat taaggaagtt attgctaatg ggataagtgt gaatgtgacg 240

ctgatattct ctcttgcaag atatgaagct gtaatagatg cttacttgga tggtcttgag 300

gcatctgggt taaatgacct ctctagagtt acaagtgttg cctctttctt tgtcagtaga 360

gtggacactc tcattgacaa ggcccttgag aaaattggca ccccagaggc tcttaatcta 420

cgtgggaagg cagc 434

<210> 616
<211> 417
<212> DNA
<213> Glycine max

<400> 616

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tgttgaagta tctcccaggc tcgctgatga cactgaggga accatagaag ctgcaaaatg 120

gcttcataaa gtggttgatc gccccaatgt gtatattaag attcctgcta cagaggcatg 180

tgtgccttca attaaggaag ttattgctaa tgggataagt gtgaatgtga cgctgatatt 240

ctctcttgca agatatgaag ctgtaataga tgcttacttg gatggtcttg aggcatctgg 300

gttaaatgac ctctctagag ttacaagggg ttgcttcttc tttgtcagta gagtggacac 360

tctcattgac aaagcccttg agaaaattgg caccccagag gctcttaatc tacgtgg 417

<210> 617
<211> 328
<212> DNA
<213> Glycine max

<400> 617

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cttgcaagat atgaagctgg ggtagatgct tacttggatg gtcttgaggc atctgggtta 120

aatgacctct ctagagttac aagtgttgcc tctttctttg tcagtagagt ggacactctc 180

attgacaagg cccttgagaa aattggcacc ccagaggctc ttaatctacg tgggaaggca 240

gcagtggccc aagcagcatt ggcttaccag cgtctccgaa ggaaatgttc tggtccaagg 300

tgggaagctc tagttaaaaa tggggcca 328

<210> 618
<211> 290
<212> DNA
<213> Zea mays

<400> 618

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acaaatgttt gtgggccgat tgcgggactg ggcaaggcat cactctggtg acccagagat 120

agatgaagct ttgaagaatg gagaagatgc tgggctttct ttggcgaaga aagtatatgc 180

ctatattcac aggattgggt acaaaacaaa gctgatggcc gctgccatac ggaacaagca 240

ggacgtattt agccttctgg ggattgatta cattattgcc cactgaagat 290

<210> 619
<211> 300
<212> DNA
<213> Zea mays

<400> 619

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aactggcaac tactcttgta attgtcattt ctaagagcgg aggcacacct gaaacccgca 120

atggtctact agaagtacag aaagccttca gagatgcggg gctgcaattc tcgaaacagg 180

gtgttgcaat tactcaagaa aattctctgt tggataacac tgctagaata gagggatggt 240

tagctcggtt tcctatgttt gattgggttg gtggtaggac ttcagaaatg tctgctgtgg 300

<210> 620
<211> 208
<212> DNA
<213> Zea mays

<400> 620

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tcccaactcc ttcctccgga acaagatcga gaccgcactc gacaaaatcc tcgccttctc 120

ccaagatgtc atctctggaa agattctttc cccatctggt cgtttcactt caattctctc 180

tataggaatc ggagggtcag ctttgggc 208

<210> 621
<211> 267
<212> DNA
<213> Zea mays

<400> 621

cccacgcgtc cgataacact gccagaatag agggatggtt agctcggttt cctatgtttg 60

actgggttgg tggtaggact tcagaaatgt cagctgttgg tttacttcca gctgcattgc 120

agtgtattga tatcaaggaa atgctatttg gtgcagcttt aatggatgag gaaacccgga 180

acactgtggt taaagcaaat ccagcagcat tgcttgcatt atgttggtat tgggcatcgg 240

aagggatagg caaaaaggat atggttg 267

<210> 622
<211> 258
<212> DNA
<213> Zea mays

<400> 622

agcttctcgc ttttttaacc acagttgtca acctaactgt cggctggaga aatggaatca 60

gagggtctgc ttatgggcct caatttgttg ctaaaccact tgcacctgat aaccctccac 120

tgaaggtaag atttattgac aacatcgatc ctggtgggat tgatcatcaa attgctcaac 180

taggatctca actggcaact agctactctt gtaattgtca tttctaagaa cacttgaggg 240

agggggaact gctgaagc 258

<210> 623
<211> 229
<212> DNA
<213> Zea mays

<400> 623

gcagaatgtg aacagggcca caactgggat tccttgaaat gttgatccag ttgacgttgc 60

acgaagcatt aaagatttgg atccagaaac cactctggtg gtggctgtat caaagacatt 120

cacaacagct gaaacaatgt taaatgctcg aactcctaag gagtggatcg tttcttctct 180

tgggacacag gctgttgcca tacatatgat tgctgtcagc actaatctt 229

<210> 624
<211> 337
<212> DNA
<213> Zea mays

<400> 624

aggttggaca gcttttatcc atctatgagc accggattgc agttcagggc ttcatatggg 60

gaattaactc atttgaccca tggggagtgg acctagggaa gtcactcgct tctcaagtga 120

ggaaacagct gcatggaacc cggatggaag gaaagcctgt tgagggtttt aaccacagca 180

cttcaagttt gcttgcacga tatcttgctg tcaagccatc caccccgtat gatactaccg 240

tgctgccgaa ggtgtaatta ctcagttgtt tttgacatgc caattgctga gctctgactt 300

ggcaaggttg agcataagtc tttcttcatt ttgggag 337

<210> 625
<211> 248
<212> DNA
<213> Zea mays

<400> 625

gcggggctgc aattctcgaa acagggtgtt gcaattactc aagaaaattc tctgttggat 60

aacactgcta gaatagaggg atggttagct cggtttccta tgtttgattg ggttggtggt 120

aggacttcag aaatgtctgc tgtgggttta cttccagctg cattgcaggg tattgatatc 180

aaggaaatgc tagctggtgc agctttaatg gatgaagaaa cccggaacac tgtggttaaa 240

gaaaatcc 248

<210> 626
<211> 288
<212> DNA
<213> Zea mays

<400> 626

gttgcaatca ctcaagaaaa ttctctgttg gataacactg ccagaataga gggatggtta 60

gctcggtttc ctatgtttga ctgggttggt ggtaggactt cagaaatgtc agctgttggt 120

ttacttccag ctgcattgca gggtattgat atcaaggaaa tgctagttgg tgcagcttta 180

atggatgagg aaacccggaa cactgtggta tcacattatt aataacacgg acaacttgca 240

gtgatggcat gattatctat atgtgtcatg tcaacatgtt tatctttt 288

<210> 627
<211> 243
<212> DNA
<213> Zea mays

<400> 627

tgatgcgggt ctgcaattct cgaaacaggg tgttgcaatc actcaagaaa attctctgtt 60

ggataacact gccagaatag agggatggtt agctcggttt cctatgtttg actgggttgg 120

tggtaggact tcagaaatgt cagctgttgg tttacttcca gctgcattgc agggtattga 180

tatcaaggaa atgctagttg gtgcagcttt aatggatgag gaaacccgga acactgtggt 240

taa 243

<210> 628
<211> 235
<212> DNA
<213> Zea mays

<400> 628

cagaaagcct tcagagatgc agggctgcaa ttctcgaaac agggtgttgc aattactcaa 60

gaaaattctc tgttggataa cactgctaga atagagggat ggttagctcg gtttcctatg 120

tttgattggg ttggtggtag gacttcagaa atgtcagctg tgggtttact tccagctgca 180

ttgcagggta ttgatatcaa ggaaatgcta gctggtgcag ctttaatgga tgagg 235

<210> 629
<211> 296
<212> DNA
<213> Zea mays

<400> 629

cgacagaatc ctcgccttct ctcaagatgt cgtctctgga aagattcttt ccccatctgg 60

tcgtttcact tcaattctct ctataggaat cggagggtca gctttgggcc ctcaatttgt 120

tgctgaggca cttgcgcctg ataaccctcc actgaagata agatttattg acaacaccga 180

tcctgctggg attgatcatc aaattgctca actaggacct gaactggcaa ctactcttgt 240

aattgtcatt tctaagagcg gaggcacacc tgaaacccgc aatgggctac tggaag 296

<210> 630
<211> 228
<212> DNA
<213> Zea mays

<400> 630

gaaagattct ttccccatct ggtcgtttca cttcaattct ctctatagga atcggagggt 60

cagctttggg ccctcaattt gttgccgagg cacttgcacc tgataaccct ccactgaaga 120

taagatttat tgacaacaca gatcctgctg ggattgatca tcaaattgct caactaggac 180

ctgaactggc aactactcgt gaaagtgaca tttctaagag cggcggca 228

<210> 631
<211> 304
<212> DNA
<213> Zea mays

<400> 631

cccacgcgtc cgccgcactc gacagaatcc tcgccttctc tcaagatgtc gtctctggaa 60

agattctttc cccatctggt cgtttcactt caattctctc tataggaatc ggagggtcag 120

ctttgggccc tcaatttgtt gctgaggcac ttgcgcctga taaccctcca ctgaagataa 180

gatttattga caacaccgat cctgctggga ttgatcatca aattgctcaa ctaggacctg 240

aactggcaac tactcttgta attgtcattt ctaagagcgg aggcacacct gaaacccgca 300

atgg 304

<210> 632
<211> 273
<212> DNA
<213> Zea mays

<400> 632

ctttatgcaa atgaccggga gtctatctct gttactgtgc aagaggtaac tcctagagct 60

gttggagcac tgattgcact ttatgaacgt gctgtgggga tttatgcttc tttggtaaat 120

atcaatgcct atcatcagcc tggtgttgag gctgggaaaa aggcagcagg agaagtattg 180

gcccttcaga aaagggttct gactgtatta aaggaggcca tctgcgagaa ccctactgag 240

ccattgactc tagatgaaat tgcagatcgc tgc 273

<210> 633
<211> 322
<212> DNA
<213> Zea mays

<400> 633

ctatcatcaa cctggtgttg aggctgggaa aaaggcagca ggagaagtgt tggcccttca 60

gaaaagggtg ctgactgtat taaatgaggc aacctgcaag gacccttgtg agccattgac 120

tatagatgaa attgcagatc gctgccattg ccctgaagat attgagatga tctacaaaat 180

agtccagcac atggctgcta acgacagagc aatcatagca gaaggcagct gtggctctcc 240

tcgcagcgtt aaggtgtacc tcggtgaatg caatgtagac gaagacttgc aggccgcgta 300

ggttccgagc ctggatccgt gt 322

<210> 634
<211> 264
<212> DNA
<213> Zea mays

<400> 634

atcaacctgg tgttgaggct gggaaaaagg cagcaggaga agtgttggcc cttcagaaaa 60

gggtgctgac tgtattaaat gaggcaacct gcaaggaccc ttgtgagcca ttgactatag 120

atgaaattgc agatcgctgc cattgccctg aagatattga gatgatctac aaaatagtcc 180

agcacatggc tgctaacgac agagcaatca tagcagaagg cagctgtggc tctcctcgca 240

gcgttaaggt gtacctcggt gaat 264

<210> 635
<211> 310
<212> DNA
<213> Zea mays

<400> 635

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ttcgacctgg atggcaaccg tgttaatcaa gggctaactg tatatggtaa caaaggaagc 120

actgaccagc atgcttacat tcagcagctg agagaaggtg tacaaaactt ctttgttacg 180

tttattgagg tcttgcgtga caggcctgct ggacatgatt ggagacttga acctggagtc 240

acgtgtggtg actatttgtt tgggatgttg cagggaaccc gttctgctct ttatgcaaat 300

gaccgggagt 310

<210> 636
<211> 295
<212> DNA
<213> Zea mays

<400> 636

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tctggatggc aaccgggtaa atcaagggct atctgtatat ggaaacaaag gaagtactga 120

ccagcacgct tacattcagc agctgagaga aggtgtacac aacttctttg ttacttttat 180

cgaggtcttg cgtgacaggc ctgctggtca tgattgggag cttgaacctg gagtcacatg 240

tggtgactat ttgtttggga tgttgcaggg aacacgttct gctctttatg caaat 295

<210> 637
<211> 293
<212> DNA
<213> Zea mays

<400> 637

acaaaggaag cactgaccag cacgcttaca ttcagcagct gagagaaggt gtacacaact 60

tctttgttac ttttatcgag gtcttgcgtg acaggcctgc tggtcatgat tgggagcttg 120

aacctggagt cacatgtggt gactatttgt ttaggatgtt gcagggaaca cgttctgctc 180

tttatgcaaa tgaccgtgaa tctatctctg ttactgtgca agaggtaact cctagagctg 240

ttggagcact ggttgcactt tatgaacgtg ctgtggggct ttatgcttct ttg 293

<210> 638
<211> 281
<212> DNA
<213> Zea mays

<400> 638

ggtgtacaaa acttctttgt tacgtttatt gaggtcttgc gtgacaggcc tgctggacat 60

gattgggagc ttgaacctgg agtcacgtgt ggtgactatt tgtttgggat gttgcaggga 120

acccgttctg ctctttatgc aaatgaccgg gagtctatct ctgttactgt gcaagaggta 180

actcctagag ctgttggagc actgattgca ctttatgaac gtgctgtggg gatttatgct 240

tctttggtaa atatcaatgc ctatcatcag cctggtgttg a 281

<210> 639
<211> 263
<212> DNA
<213> Zea mays

<400> 639

ccggaacact gtggttaaag aaaatccagc agcattgctt gcattatgtt ggtattgggc 60

atcagaaggg ataggcaata aggatatggt tgtacttcct tacaaggata gtttgttgct 120

tttgagtaga tatttgcaac aacttgtcat ggaatctctt gggaaagaat ttgatctgga 180

tggcaaccgg gtaaatcaag ggctatctgt atatggaaac aaaggaagca ctgaccagca 240

cgcttacatt cagcagctga gag 263

<210> 640
<211> 300
<212> DNA
<213> Zea mays

<400> 640

cggacgcgtg gtgctagctg gtgcagcttt aatggatgag gaaacccgga acactgtggt 60

taaagaaaat ccagcagcat tgcttgcatt atgttgctat tgggcatcag aagggatagg 120

caataaggat atggttgtac ttccttacaa ggatagtttg ttgcttttga gtagatattt 180

gcaacaactt gtcatggaat ctcttgggaa agaatttgat ctggatggca accgggtaaa 240

tcaagggcta tctgtatatg gaaacaaagg aagcactgac cagcacgctt acattcagca 300

<210> 641
<211> 313
<212> DNA
<213> Zea mays

<400> 641

cccacgcgtc cgcccacgcg tccggggtat tgatatcaag gaaatgctag ctggtgcagc 60

tttaatggat gaagaaaccc ggaacactgt ggttaaagaa aatccagcag cattgcttgc 120

attatgttgg tattgggcat cagaagggat aggcaataag gatatggttg tacttcctta 180

caaggatagt ttgttgcttt tgagtagata tttgcaacaa cttgtcatgg aatctcttgg 240

gaaagaattt gatctggatg gcaaccgggt aaatcaaggg ctatctgtat atggaaacaa 300

aggaagtact gac 313

<210> 642
<211> 298
<212> DNA
<213> Zea mays

<400> 642

gatagtttgt tacttttgag tagatatttg cctatccctt ccgatgccca ataccagcag 60

cattgcttgc attatgttgg tattgggcat cggaagggat aggcaaaaag gatatggttg 120

tgcttcctta taaggatagt ttgttacttt tgagtagata tttgcaacaa cttgtcatgg 180

gatctcttgg aaaagaattc gacctggatg gcaaccgtgt taaacaaggg ctaactgtat 240

atggtaacaa aggaagcact gaccagcatg cttacattca gcagctgaga gaaggtgt 298

<210> 643
<211> 274
<212> DNA
<213> Zea mays

<400> 643

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ggtgactatt tgtttgggat gttgcaggga acccgttctg ctctttatgc aaatgaccgg 120

gagtctatct ctgttacgtg caagaggtaa ctcctagagc tgttggagca ctgatttcac 180

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ctggtgttga ggctgggaaa aaggcagcag gaga 274

<210> 644
<211> 284
<212> DNA
<213> Zea mays

<400> 644

cagctgcatt gcagggtatt gatatcaagg aaatgctagc tggtgcagct ttaatggatg 60

aggaaacccg gaacactgtg gttaaagaaa atccagcagc attgcttgca ttatgttggt 120

attgggcatc agaagggata ggcaataagg atatggttgt acttccttac aaggatagtt 180

tgttgctttt gagtagatat ttgcaacaac ttgtcatgga atctcttggg aaagaatttg 240

atctggatgg caaccgggta aatcaaggct atctgtatat ggaa 284

<210> 645
<211> 306
<212> DNA
<213> Zea mays

<400> 645

cggacgcgtg gtgctagctg gtgcagcttt aatggatgag gaaacccgga acactgtggt 60

taaagaaaat ccagcagcat tgcttgcatt atactggtat tgggcatcag aagggatagg 120

caataaggat atggttgtac ttccttacaa ggatagtttg ttgcttttga gtagatattt 180

gcaacaactt gtcatggaat ctcttgggaa agaatttgat ctggatggca accgggtaaa 240

tcaagggcta tctgtatatg gaaacaaagg aagcactgac cagcacgctt acattcagca 300

gctgag 306

<210> 646
<211> 271
<212> DNA
<213> Zea mays

<400> 646

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tggtcatgaa tgggagcttg aacctggagt cacatgtggt gactatttgt ttgggatgtt 120

gcagggaaca cgttctgctc tttatgcaaa tgaccgtgaa tctatctctg ttactgtgca 180

agaggtaact cctagagctg ttggagcact ggttgcactt tatgaacgtg ctgtggggct 240

ttatgcttct ttggtaaata tcaatgccta t 271

<210> 647
<211> 228
<212> DNA
<213> Zea mays

<400> 647

cggacgcgtg gggtgtaca caacttcttt gttacgttta ttgaggtctt gcgtgacagg 60

cctgctggtc atgattggga gcttgaacct ggagtcacgt gtggtgacta tttgtttggg 120

atgttgcagg gaacccgttc tgctctttat gcaaatgacc gggagtctat ctctgttact 180

gtgcaagagg taactcctag agctgttgga gcactgattg cactttat 228

<210> 648
<211> 275
<212> DNA
<213> Zea mays

<400> 648

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tgattgggag cttgaacctg gagtcacatg tggtgactat ttgtttggga tgttgcaggg 120

aacacgttct gctctttatg caaatgaccg tgaatctatc tctgttactg tgcaagaggt 180

aactcctaga gctgttggag cactggttgc actttatgaa cgtgctgtgg ggctttatgc 240

ttcttggtaa atatcaatgc tatcatcaac tggtg 275

<210> 649
<211> 203
<212> DNA
<213> Zea mays

<400> 649

tgttgtactt ccttacaagg atagtttgtt gcttttgagt agatatttgc aacaacttgt 60

catggaatct cttgggaaag aatttgatct ggatggcaac cgggtaaatc aagggctatc 120

tgtatatgga aacaaaggaa gcactgacca gcacgcttac attcagcagc tgagagaagg 180

tgacacaact tctttgttac ttt 203

<210> 650
<211> 285
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 650

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cccggaacac tgtggttaaa gaaaatccag cagcattgct tgcattatgt tggtattggg 120

catcagaagg gataggcaat aaggatatgg ntgtacttcc ttacaaggat agtttgttgc 180

ttttgagtag atatttgcaa caacttgtca tggaatctct tgggaagaat tgatctggat 240

gcaaccggta aatcaaggct atctgatatg aaacaaagaa gactg 285

<210> 651
<211> 267
<212> DNA
<213> Zea mays

<400> 651

tatcttgctg tcaagccatc caccccgtat gatactaccg tgctgccgaa gtgtaattac 60

tcagttgttt ttgacatgcc aattgctgag ttctgacttg gcaaggttga gcataagtct 120

ttcttcattt tgggagttat cacagagcca gtttggcagt gctgtagttt tggttttacc 180

tactctttgt agaagaaaag tgaagagtgg atattatgga acaaaatata tacctacggc 240

agcacgcagc atgatgaaac atattta 267

<210> 652
<211> 240
<212> DNA
<213> Zea mays

<400> 652

gtctcccccg accggcgatc gctatcgact tgtagcggaa gccatggcgt cggcagcgct 60

aatctgcggc acggagcagt ggaaggccct ccaggcgcac gtcggcgcga ttcagaagac 120

gcacctgcgc gacctgatgg ccgacgccga ccgatgcaag gcaatgacgg ctgagtatga 180

agggatcttt ctggattact cgagacagca ggcgactggt gaaacatgga gaagccctta 240

<210> 653
<211> 292
<212> DNA
<213> Zea mays

<400> 653

caaaatccgg aggaactccc aggaggcgaa aagcagatcc gtctcccccg agccccgacc 60

ggcgatcgct atcgacttgt agcggaagcc atggcgtcgg cagcgctaat ctgcggcacg 120

gagcagtgga aggccctcca ggcgcacgtc ggcgcgattc agaagacgca cctgcgcgac 180

ctgatggccg acgccgaccg atgcaaggca atgacggctg agtatgaagg gatctttctg 240

gattactcga gacagcaggc gactggtgaa acatggagaa gctcttaaat tg 292

<210> 654
<211> 320
<212> DNA
<213> Zea mays

<400> 654

ggcaagcaaa cgagcggcgg gacggctagc ccgcaataca aaatccggag gaactcccag 60

gaggcgaaaa gcagatccgt ctcccccgag ccccgaccgg cgatcgctat cgacttgtag 120

cggaagccat ggcgtcggca gcgctaatct gcggcacgga gcagtggaag gccctccagg 180

cgcacgtcgg cgcgattcag aagacgcacc tgcgcgacct gatggccgac gccgaccgat 240

gcaaggcaat gacggctgag tatgaaggga tctttctgga ttactcgaga cagcaggcga 300

ctggtgaaac catggagaag 320

<210> 655
<211> 278
<212> DNA
<213> Zea mays

<400> 655

caccgtcttc cggccgtcca ccgtttccag cacacagggt aaaggcaagc aaacgagcgt 60

ggggacggct agcccgcaat acaaaatccg gaggaactct caggaggcga aaagcagatc 120

tgtctccccc gaccggcgat cgctatcgac ttgtagcgga agccatggcg tcggcagcgc 180

taatctgcgg cacggagcag tggaaggcac tccaggcgca cgtcggcgcg attcagaaga 240

cgcaactgcg cgacctgatg gccgacgccg accgatgc 278

<210> 656
<211> 105
<212> DNA
<213> Zea mays

<400> 656

caaaatccgg aggaactccc aggaggcgaa aagcagatcc gtctccccccg agccccgacc 60

ggcgatcgct atcgacttgt agcggaagcc atggcgtcgg cagcg 105

<210> 657
<211> 267
<212> DNA
<213> Zea mays

<400> 657

acccgatcaa gctgtgggag cgctacgtcg agtggctcta ccagcacaag gagctcggca 60

tcttcgtcga cgtcagccgg atggggttca cggaggagtt cctgcggcag atggagccgc 120

ggatgcagca ggccttcgtc gacatgcggg agctcgagaa gggcgccatc gccaaccccg 180

acgagggtcg catggtgggc cactactggc tccgcgaccc ggccctcgct cccaactcct 240

tcctccggaa caagatcgag accgcac 267

<210> 658
<211> 325
<212> DNA
<213> Zea mays

<400> 658

tgccatattc tcaggcactt gagaagttgg caccacatat acagcagctt agcatggaga 60

gtaacgggaa gggtgtttcc attgatggcg cccaactttc ctttgagaca ggtgaaattg 120

attttggtga acctcgaact aatggccagc acagcttcta tcaattaatc catcagggaa 180

gggttatccc ttgcgacttt attggtgttg ttaaaagtca gcagcctgtt tacttgaaag 240

gggaaactgt gagtaatcat gatgagctta tgtccaattt ctttgcccaa cctgatgctc 300

ttgcttatgg aaagactcct gaaca 325

<210> 659
<211> 316
<212> DNA
<213> Zea mays

<400> 659

tccagctagg gcaatattgc catattctca ggcacttgag aagttggcac cacatataca 60

gcagcttagc atggagagta acgggaaggg tgtttccatt gatggcgccc aactttcctt 120

tgagacaagt gaaattgatt ttggtgaacc tggaactaat ggccagcaca gcttctatca 180

attaatccat cagggaaggg ttatcccttg cgactttatt ggtgttgtta aaagtcagca 240

gcctgtttac ttgaaagggg aaactgtgag taatcatgat gagcttatgt ccaatttctt 300

tgcccaacct gatgct 316

<210> 660
<211> 300
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 660

atcaaagaca ttcacaacag ctgnaaacaa tgttaaatgc tcgaactctt aaggagtgga 60

tcgtttcttc tcttgggcca caggctgttg ccaaacatat gattgctgtc agcactaatc 120

ttaagcttgt gaaggagttt ggaattgacc caaacaatgc ttttgccttt tgggactggg 180

ttggcggccg ttatagtgtt tgcagtgctg ttggcgttct gccattatct cttcagtatg 240

gctttccaat tgtccagaaa tttttggagg gagcttccag tatcgacaac cacttctact 300

<210> 661
<211> 334
<212> DNA
<213> Zea mays

<400> 661

ctcatgatga gcttatgtcc aatttctttg cccaacctga tgctcttgct tatggaaaga 60

ctcctgaaca gttgcacagt gagaaagttc cagataatct tatccctcat aagactttta 120

agggcaaccg gccatcacta agtttgcttc tgcctacact atctgcatat gaggttggac 180

agcttttatc catctatgag caccggattg cagttcaggg cttcatatgg ggaattaact 240

catttgacca ctagggagtg gagctaggga agtcactcgc ttctcaagtg aggaaacagc 300

tgcatggaac ccggatggaa ggacacctgt tgag 334

<210> 662
<211> 279
<212> DNA
<213> Zea mays

<400> 662

ggtgaacctg gaactaatgg ccagcacagc ttctatcaat taatccatca gggaagggtt 60

atcccttgcg actttattgg tgttgttaaa agtcagcagc ctgtttactt gaaaggggaa 120

actgtgagta atcatgatga gcttatgtcc aatttctttg cccaacctga tgctcttgct 180

tatggaaaga ctcctgaaca gttgcacagt gagaaagttc cagaaaatct tatccctcat 240

aagactttta agggcaaccg gccatcacta agtttgctt 279

<210> 663
<211> 274
<212> DNA
<213> Zea mays

<400> 663

tgcaaatgtt gatccagttg acgttgcacg aagcattaaa gatttggatc cagaaaccac 60

tctggtggtg gttgtatcaa agacattcac aacagcggaa acaatgttaa atgctcgaac 120

tcttaaggag tggatcgttt cttctcttgg gccacaggct gttgccaaac atatgattgc 180

tgtcagcact aatcttaagc ttgtgaagga gtttggaatt gacccaaaca atgcttttgc 240

cttttgggac tgggttggcg gccgttatag tgtt 274

<210> 664
<211> 283
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 664

gccacaggct gttgccaaac atatgattgc tgtcagcact aatcttaagc ttgtgaagga 60

gtttggaatt ganccaaaca atgcttntgc ctnttgggac tgggttggcg gccgttatag 120

tgtttgcagt gctgttggcg ttctgccatt atctcttcag tatggcttgc caattgtcca 180

gaaatttttg gagggagctt ccagcattga caaccactnc tactcatctt catgtgagaa 240

naatataccn gtacntcttg gtgctgagtg tgtggaatgt ttc 283

<210> 665
<211> 269
<212> DNA
<213> Zea mays

<400> 665

gccacaggct gttgccaaac atatgattgc tgtcagcact aatcttaagc ttgtgaagga 60

gtttggaatt gacccaaaca atgcttttgc cttttgggac tgggttggcg gccgttatag 120

tgtttgcagt gctgttggcg ttctgccatt atctcttcag tatggctttc caattgtcca 180

gaaatttttg gagggagctt ccagcattga caaccacttc tactcatctt catttgagaa 240

aaatataccg tacttcttgg tttgctgag 269

<210> 666
<211> 299
<212> DNA
<213> Zea mays

<400> 666

agaagtggat catgggttgg agcaactgga aaaccgttga caaatgttgt gtcagttgga 60

ataggtggta gctttcttgg ccctctattt gtgcatactg cactccagac cgatccagaa 120

gcagcagaat gtgcaaaagg ccggcaactg agattccttg caaatgttga tccagttgac 180

gttgcacgaa gcattaaaga tttggatcca gaaaccactc tggtggtggt tgtatcaaag 240

acattcacaa cagctgaaac aatgttaaat gctcgaactc ttaaggagtg gatcgtttc 299

<210> 667
<211> 276
<212> DNA
<213> Zea mays

<400> 667

ttggaattga cccaaacaat gcttttgcct tttgggactg ggttggcggc cgttatagtg 60

tttgcagtgc tgttggcgtt ctgccattat ctcttcagta tggctttcca attgtccaga 120

aatttttgga gggagcttcc agcattgaca accacttcta ctcatcttca tttgagaaaa 180

atatacctgt acttcttggt ttgctgagtg tgtggaatgt tcatttcttg gttatccagc 240

tagggcaata tgccatatct caggcacttg agaagt 276

<210> 668
<211> 255
<212> DNA
<213> Zea mays

<400> 668

ctccaagaga tgcagtcata aacagtgatg gggtgactgt ggtccctgag gtttggagtg 60

ttaaagataa aatcaagcag ttttcagaga cttttagaag tggatcatgg gttggagcaa 120

ctggaaaacc gttgacaaat gttgtgtcgg ttggaatagg tggtagcttt cttggccctc 180

tatttgtgca tactgcactc cagaccgatc cagaagcagc agaatgtgca aaaggccggc 240

aactgagatt ccttg 255

<210> 669
<211> 233
<212> DNA
<213> Zea mays

<400> 669

gcacgaggtt ctgccattat ctcttcagta tggctttcca attgtccaga aatttttgga 60

gggagcttcc agcattgaca accacttcta ctcatcttca tttgagagaa atatacctgt 120

acttcttggt ttgctgagtg tgtggaatgt ttcatttctt ggttatccag ctagggcaat 180

attgtcatat tctcaggcac ttgagaagtt ggcaccacat atacagcagc tta 233

<210> 670
<211> 191
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 670

aatttctttg cccaacctga tgctcttgct tatggaaaga ctcctgaaca gttgcacagt 60

gagaaagttc cagaaaatct tatccctcat aagactttta agggcaaccg gccatcacta 120

agtttgcttc tgcctacact atccgcatat gaggtggaca gttttaancc tctatngggc 180

ncggtttnan t 191

<210> 671
<211> 115
<212> DNA
<213> Zea mays

<400> 671

gtggtagctt tcttggccct ctatttgtgc atactgcact ccagaccgat gcagaagcag 60

cagaatgtgc aaaaggccgg caactgagat tccttgcaaa tgttgatcca gttga 115

<210> 672
<211> 113
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 672

ggagtttgga attgacccaa acaatgcttt tgccttttgg gactgggttg gcggccgtta 60

tagtgtttgc agtgctgttg gcgntctgcc attatctctt cagtatggct ttc 113

<210> 673
<211> 122
<212> DNA

<213> Zea mays

<400> 673

tatcttatcc ctcataagac ttttaagggc aaccggccat cactaagttt gcttctgcct 60

acactatctg catacgaggt tacgacagct tttatccatc tatgagcacc ggattgcagt 120

tc 122

<210> 674
<211> 443
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 674

agtctatctc tgttactgtg caagaggtaa ctcctanagc tgttggagna ctgattgcac 60

tttatgaacg tgctgtgggg atttatgctt ctttggtaaa tatcaatgcc tatcatcagc 120

ctggtgttga ggctgggaaa aaggcancan gagaagtatt ggcccttcag aaaagggttc 180

tgactgtatt aaaggaggcc atctgcnaga accctactga gccattgact ctagatgaaa 240

ttgcagatcg ctgacattgc cctgaagata ttganatgat ctacanaata atccancaca 300

tggcttctaa cgacagatca cttatagcag aaggcatctg cngctttctt ngcagtgtta 360

aggtgtacct nggtgaaatg caattttgga ccnaantatg caggccggga tagattctgn 420

gtcnggancn aagtaacatt ntt 443

<210> 675
<211> 420
<212> DNA
<213> Zea mays

<400> 675

ctcttgggaa agaatttgat ctggatggca accgggtaaa tcaagggcta tgtgtagatg 60

gaaacaaagg aagcactgac cagcacgctt acattcagca gctgagagaa ggtgtacaca 120

acttctttgt tacttttatc gaggtcttgc gtgacaggcc tgctggtcat gattgggagc 180

ttgaacctgg agtcacatgt ggtgactatt tgtttgggat gttgcaggga acacgttctg 240

ctctttatgc aaatgaccgt gaatctatct ctgttactgt gcaagaggta actcctagag 300

ctgttggagc actggttgca ctttatgaac gtgctgtggg gctttatgct tctttggtaa 360

atatcaatgc ctatcatcaa cctggtgttg aggctgggaa aaaggcagca ggagaagtgt 420

<210> 676
<211> 349
<212> DNA
<213> Zea mays

<400> 676

tgcggtcaag caatcaaccc cgtatgatac aaccgtgctg ccgaaggtgt aattacccag 60

ttgtttttga catgccaatt gctgagttct gacttggcaa ggttgagcat aagtctttct 120

tcatttggga gttatcacag agccagtttg gcagtgctgt agttttggtt ttacctactc 180

tttgtagaag aaaagtgaag agtggatatt atggaacaaa atatatacct acggcagcac 240

gcagcatgat gaaacatatt taaaaaattt gggtgctcta ccacatgccc gtggaataaa 300

acggatgtaa actcagtgca aaaaaaaaaa aaaaaaaaaa aaacaaaaa 349

<210> 677
<211> 376
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 677

aacgagcggc gggacggcta gcccgcaata caaaatccgg aggaactccc aggaggcgaa 60

aagcagatcc gtctccccg agccccgacc ggcgatcgct atcgacttgt agcggaagcc 120

atggcgtcgg cagcgctaat ctgcggcacg gagcagtgga aggccctcca ggcgcacgtc 180

ggcgcgattc agaagacgca cctgcgcgac ctgatggccg acgccgaccg atgcaaggca 240

atgacggctg agtatgaagg gatctttctg gattactcga gacagcaggc gactggtgaa 300

accctggaga agctccttaa atgggctgac gctgcgaagc tcaaggagaa ngatgagaag 360

atgtttaaag gtgaaa 376

<210> 678
<211> 451
<212> DNA
<213> Zea mays

<400> 678

ccgtatatag tgtttgcagt gctgttggcg ttctgccatt atctcttcag tatggctttc 60

caattgtcca gaaatttttg gagggagctt ccagcattga caaccacttc tactcatctt 120

catttgagaa aaatatacct gtacttcttg gtttgctgag tgtgtggaat gtttcatttc 180

ttggttatcc agctagggca atattgccat attctcaggc acttgagaag ttggcaccac 240

atatacagca gcttagcatg gagagtaacg ggaagggtgt ttccattgat ggcgcccaac 300

tttcctttga gacaggtgaa attgattttg gtgaacctgg aactaatggc cagcacagct 360

tctatcaatt aatccatcaa ggaagggtta tcccttgcga ctttattggt gttgttaaaa 420

gtcagcagcc tgtttacttg aaaagggaaa c 451

<210> 679
<211> 453
<212> DNA
<213> Zea mays

<400> 679

gtcatgcact ggagacgttg gcactacata tacagcagct tatcatggat agtaacgggg 60

ggggtgtttc cattgatggc gcccaacttt cctttgagac aggtgaaatt gattttggtg 120

aacctggaac taatggccag cacagcttct atcaattaat ccatcaggga agggttatcc 180

cttgcgactt tattggtgtt gttaaaagtc agcagcctgt ttacttgaaa ggggaaactg 240

tgagtaatca tgatgagctt atgtccaatt tctttgccca acctgatgca cttgcttatg 300

gaaagactcc tgaacagttg cacagtgaga aagttccaga aaatcttatc cctcataaga 360

cttttaaggg caaccggcca tcactaagtt tgcttctgcc tacactatcc gcatatgagg 420

ttggacagct tttatccatc tatgagcacc gga 453

<210> 680
<211> 419
<212> DNA
<213> Zea mays

<400> 680

aaaatcaagc agttttcaga gacttttaga agtggatcat gggttggagc aactggaaaa 60

ccgttgacaa atgttgtgtc agttggaata ggtggtagct ttcttggccc tctatttgtg 120

catactgcac tccagaccga tccagaagca gcagaatgtg caaaaggccg gcaactgaga 180

ttccttgcaa atgttgatcc agttgacgtt gcacgaagca ttaaagattt ggatccagaa 240

accactctgg tggtggttgt atcaaagaca ttcacaacag ctgaaacaat gttaaatgct 300

cgaactctta aggagtggat cgtttcttct cttgggccac aggctgttgc caaacatatg 360

attgctgtca gcactaatct taagcttgtg aaggagtttg gaattgaccc aaacaatgc 419

<210> 681
<211> 426
<212> DNA
<213> Zea mays

<400> 681

ctcgcgggcc gacacacgcc tctacatttc ttggttatac agctagggca atattgccat 60

attctcaggc acttgagaag ttggcaccac atatacagca gcttagcatg gagagtaacg 120

ggaagggtgt ttccattgat ggcgcccaac tttcctttga gacaggtgaa attgattttg 180

gtgaacctgg aactaatggc cagcacagct tctatcaatt aatccatcag ggaagggtta 240

tcccttgcga ctttattggt gttgttaaaa gtcagcagcc tgtttacttg aaaggggaaa 300

ctgtgagtaa tcatgatgag cttatgtcca atttctttgc ccaacctgat gctcttgctt 360

atggaaagac tcctgaacag ttgcacagtg agaaagttcc agaaaatctt atccctcata 420

agactt 426

<210> 682
<211> 323
<212> DNA
<213> Zea mays

<400> 682

gcgaagctca aggagaagat tgagaagatg tttaaaggtg aaaagataaa tagcacagag 60

aacaggtcag tgcttcatgt agctctgagg gctccaagag atgcagtcat aaacagtgat 120

ggggtgaatg tggtccctga ggttcggagt gttaaagata aaatcaagca gttttcagag 180

acttttagaa gtggatcatg ggttggagca actggaaaac cgttgacaaa tgttgtgtcg 240

gttggaatag gtggtagctt tcttggccct ctatttgtgc atactgcact ccagaccgat 300

ccagaagcag cagaatgtgc aaa 323

<210> 683

<211> 422
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 683

ccaaaactga gtctcattac aaatgtngat cnanttgacg ttgcacnaan cattaaagat 60

ttggntccag aaaccacccn ggtggtggtt gtancaaaga cattcacaac agcggaaaca 120

atgttaaatg ctcgaactct taaggagtgg atcgtttctt ctcttgggcc acaggctgtt 180

gccaaacata tgattgctgt cagcactaat cttaagcttg tgaaggagtt tggaattgac 240

ccaaacaatg cttttgcctt ttgggactgg gttggcggcc gttatagtgt ttgcagtgct 300

gttggcgttc tgccattact cttcagtatg gctttccaat tgtccagaaa tttttggagg 360

gaacttccag ncattgacaa acaacttcna ntcnncctnc attttgagaa aaatatacct 420

gt 422

<210> 684
<211> 122
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 684

ggtgagtaac catgatgagc taatgtccaa ctattttgca cagtctgatg cccttgcata 60

tnnnaagaca gcagagcagc tgcnaaaggn caatgtttcc ccgcacctta ttccacacaa 120

ga 122

<210> 685
<211> 234
<212> DNA
<213> Glycine max

<400> 685

tgataatcct ccactcaaga taacatacat ggacaacacg gatcctgctg gaattgatca 60

tcagattgca caacttgggc ctgagctagc ttcaacactt gtgattgtga tatcaaagag 120

tggaggtact cctgagacca gaaatggttt attggaagtg cagaaggcct ttcgtgaagc 180

aggcttggat tttcctaaac agggtgttgc tataacacaa gaaaattctt tgtt 234

<210> 686
<211> 205
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 686

ttcctatgtt tgatnggnnn ggaggtagaa cgtcagnnat gtctgcagtt ggcctgcttc 60

cagcagccct tccagggatt ganatnanag aaatgcttgc cggtgcatca ttgatggatg 120

angctaanag gagtactgtg nnaaggaata accctgcagc tctgctggct ttatgttggt 180

attgggctac agatggtgna ggatc 205

<210> 687
<211> 223
<212> DNA
<213> Glycine max

<400> 687

tgcagggcgt tgctataact caagaaaatt ctttgctgga taacactgca agaattgagg 60

gttggttagc tagatttcca atgtttgact gggtgggagg tagaacatca gagatgtctg 120

cagtgggcct gcttccagca gcccttcaga gcattgacat aagagaaatg cttgctggtg 180

cagcattaat ggatgaggcg aataggagta ctgtgataag gaa 223

<210> 688
<211> 218
<212> DNA
<213> Glycine max

<400> 688

tgcagggcgt tgctataact caagaaaatt ctttgctgga taagactgca agaattgacg 60

gttggttagc tagatttcca atgtttgact gggtgggagg tagaacatca gagatgtctg 120

cagtgggcct gcttccagca gcccttcaga gcattgacat aagagaaatg cttgctggtg 180

cagcattaat ggatgaggcg aataggagta ctgtgata 218

<210> 689
<211> 274
<212> DNA
<213> Glycine max

<400> 689

gtgctacgtg atagacctcc tggtcatgat tgggaacttg aacctggtgt ccacatgcgg 60

tgactacttg tttggtatgc tacagggaac aagatcagct ctgtatgcca ataaccgaga 120

gtccatcaca gttactgtac aagaagtgac acctagaaca gttggtgctc ttattgcact 180

ctatgaacga gcagtaggaa tttatgcctc ccttgtcaac ataaatgctt atcatcaacc 240

aggtgtggaa gctggtaaaa aagcagcagg tgaa 274

<210> 690
<211> 257
<212> DNA
<213> Glycine max

<400> 690

aacaattgag ggaaggtgta cacaatttct ttgtaacatt cattgaggtg ctacgtgata 60

gacctcctgg tcatgattgc gaacttgaac ctggtgtcac atgcggtgac tacttgtttg 120

gtatgctaca gggaacaaga tcagctctgt atgccaataa ccgagagtcc atcacagtta 180

ctgtacaaga agtgacacct agaactgttg gtgctcttat tgcactctat gaacgagcag 240

taggaattta tgcctcc 257

<210> 691
<211> 251
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 691

gattgggaac ttgaacctgg tgtcacatgt ggtgactact tgtttggtat gctacaggga 60

acaaggtcgg ctttgtatgc caataaccga gagtccatca cagttactgt acaagaaggg 120

acaccaagaa cagttggtgc tcttattggg ctctatgaac gagcagtagg aatttatgcc 180

tcccctgtca acataaatgc ttatctnaac ctgcgtgtgg aagntgacga natnagcagc 240

agngaagtac t 251

<210> 692
<211> 245
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 692

atcctgcanc tttgcnggct ttatgttggt attgggctac agatggtgta ngatcaaaag 60

atatggttat ccttccatat aaggacagct nganattatn tagtagatac ttgcaacagt 120

nggtcatgga atctctaggc aaggagtttg actgaatggt aatcgggtta atcaaggaat 180

tagtgtctat ggaaataaag gaagcacaga tcagcatgcc tacatccaac aactgaggga 240

aggtg 245

<210> 693
<211> 270
<212> DNA
<213> Glycine max

<400> 693

cagcatgcct acattcagca actgagggaa ggtgtgcaca atttttttgt gacattcatt 60

gaggtgctac gcgatagacc acctggtcat gattgggagc ttgaaccagg tgtcacatgt 120

ggtgactacc tgtttggtat gctacaggga acaaggtcag ccctgtatgc caataaccgt 180

gaatccatca ctgtcacagt gcaagaagtg acacccagat cagttggtgc ccttgtagcc 240

ctttatgaac gggccgttgg aatatatgct 270

<210> 694
<211> 259
<212> DNA
<213> Glycine max

<400> 694

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gacattcatt gaggtgctac gcgatagacc acctggtcat gattgggagc ttgaaccagg 180

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<210> 695
<211> 227

<212> DNA
<213> Glycine max

<400> 695

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<210> 696
<211> 263
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 696

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cagatggtgt aggaccaagg anatggttat tcttccgtac aaggacagcc tngtattatt 180

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taatcgggtt aatcaaggaa tag 263

<210> 697
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<212> DNA
<213> Glycine max

<400> 697

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agttcgctaa cgacgtcgtt agtggtaaga ttaagcctcc ttcgtctccg gagggtcgat 180

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<210> 698
<211> 398
<212> DNA

<213> Glycine max

<223> unsure at all n locations
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aaaggaagca cagatcagca tgcctacatt cagcaactga nggaaggtgt gcacaatttt 300

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caagtgtcac atgtggtgac tacctgtttg gtatgcta 398

<210> 699
<211> 362
<212> DNA
<213> Glycine max

<400> 699

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ac 362